

O'Bryen, Barbara

From: Hale, Mary
Sent: Tuesday, May 10, 2005 9:40 AM
To: Wacławiw, Alexandra; O'Bryen, Barbara; Shears, Beverly; Schreiber, David; Arnold, Deirdre; Hart, Edward; Delaval, Jan; Ruhl, Mary Jane; Jarrell, Noble; Schulwitz, Paul; Sheppard, Paula; Port, Toby
Subject: FW: sequence search

If you have this search please let me know and contact Bridget with the status.

Thanks,
Mary

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Tuesday, May 10, 2005 9:36 AM
To: Hale, Mary
Subject: FW: sequence search

Mary Ms. Bunner inquired about this search, it has been logged in but not completed.

-----Original Message-----

From: Bunner, Bridget
Sent: Wednesday, April 27, 2005 4:12 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/892,360 (please include the pending databases):

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

*Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70*

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:22:27 ; Search time 43 Seconds
(without alignments)
933.981 Million cell updates/sec

Title: US-09-892-360-2
Perfect score: 2760
Sequence: 1 MFPLYTDFFLSLVAVPAAP.....IPTDKREPENNILLEDRN 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2760	100.0	538	4	US-09-949-016-7001 Sequence 7001, Ap
2	2760	100.0	538	4	US-09-949-016-7368 Sequence 7368, Ap
3	1248.5	45.2	411	3	US-09-236-080-6 Sequence 6, Appli
4	1242.5	45.0	411	3	US-09-236-080-2 Sequence 2, Appli
5	1242.5	45.0	411	3	US-09-336-643A-83 Sequence 83, Appl
6	1238.5	44.9	370	3	US-09-144-914-8 Sequence 8, Appli
7	822.5	29.8	419	4	US-09-949-016-6913 Sequence 6913, Ap
8	822.5	29.8	440	4	US-09-949-016-7809 Sequence 7809, Ap
9	812.5	29.4	393	4	US-09-432-470-2 Sequence 2, Appli
10	812.5	29.4	393	4	US-09-432-470-2 Sequence 4, Appli
11	483	17.5	499	4	US-09-561-763-2 Sequence 2, Appli
12	483	17.5	499	4	US-09-431-367B-2 Sequence 2, Appli
13	447	16.2	107	3	US-09-236-080-4 Sequence 2, Appli
14	403	14.6	336	3	US-08-749-816-2 Sequence 2, Appli
15	403	14.6	336	3	US-09-144-914-2 Sequence 2, Appli
16	396	14.3	332	4	US-09-561-763-5 Sequence 5, Appli
17	396	14.3	332	4	US-09-431-367B-5 Sequence 5, Appli
18	361	13.1	361	4	US-09-362-842-14 Sequence 14, Appl
19	352.5	12.8	405	3	US-09-144-914-5 Sequence 5, Appli
20	349.5	12.7	394	3	US-09-144-914-4 Sequence 4, Appli
21	342	12.4	388	4	US-09-949-016-7631 Sequence 7631, Ap
22	333.5	12.1	313	3	US-09-336-643A-81 Sequence 81, Appl
23	333.5	12.1	313	4	US-09-561-763-8 Sequence 8, Appli
24	333.5	12.1	313	4	US-09-431-367B-8 Sequence 8, Appli
25	323	11.7	408	4	US-09-362-842-12 Sequence 12, Appl
26	295.5	10.7	273	4	US-09-949-016-7794 Sequence 7794, Ap
27	290.5	10.5	618	1	US-08-332-312-2 Sequence 2, Appli

28	287	10.4	257	4	US-09-949-016-6654 Sequence 6654, Ap
29	233.5	8.5	995	4	US-09-362-842-2 Sequence 2, Appli
30	233	8.4	395	4	US-09-362-842-6 Sequence 6, Appli
31	220	8.0	401	4	US-09-561-763-11 Sequence 11, Appl
32	220	8.0	401	4	US-09-431-367B-11 Sequence 11, Appl
33	212.5	7.7	336	1	US-08-332-312-4 Sequence 4, Appli
34	197	7.1	730	4	US-09-362-842-4 Sequence 4, Appli
35	197	7.1	741	4	US-09-362-842-67 Sequence 67, Appl
36	197	7.1	741	4	US-09-270-767-45442 Sequence 45442, A
37	186.5	6.8	1153	4	US-09-362-842-8 Sequence 8, Appli
38	164.5	6.0	347	3	US-08-749-816-3 Sequence 3, Appli
39	164.5	6.0	347	3	US-09-144-914-6 Sequence 6, Appli
40	162	5.9	308	4	US-09-248-796A-20134 Sequence 20134, A
41	159	5.8	383	3	US-08-749-816-4 Sequence 4, Appli
42	159	5.8	383	3	US-09-144-914-7 Sequence 7, Appli
43	137.5	5.0	146	4	US-09-362-842-69 Sequence 69, Appl
44	137.5	5.0	146	4	US-09-270-767-31685 Sequence 31685, A
45	134	4.9	197	3	US-09-336-643A-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-7001
; Sequence 7001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7001
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7001

Query Match	100.0%	Score 2760;	DB 4;	Length 538;
Best Local Similarity	100.0%	Pred. No. 1.3e-246;	Mismatches 0;	Indels 0;
Matches 538;	Conservative 0;			Gaps 0;
QY	1	MFPLYTDFFLSLVAVPAAPVCQPKSATNGQPPAPPTPTPLRSISSRATVVARMEGTSQ	60	
Db	1	MFPLYTDFFLSLVAVPAAPVCQPKSATNGQPPAPPTPTPLRSISSRATVVARMEGTSQ	60	
QY	61	GGLOTVMKTKVVAIFVWVYLVLTGGLVFPALQPPFESSOKNTIALEKAEFLRDHVCVS	120	
Db	61	GGLOTVMKTKVVAIFVWVYLVLTGGLVFPALQPPFESSOKNTIALEKAEFLRDHVCVS	120	
QY	121	POELETLIQHALDADNAGVSPIGNSSNNSSNWDLSGSAFFAGTGTITTYGNIAPSTEGG	180	
Db	121	POELETLIQHALDADNAGVSPIGNSSNNSSNWDLSGSAFFAGTGTITTYGNIAPSTEGG	180	
QY	181	KIFCILYAIIFGIFLFGLAGIGDQGTIFGKSIAARVEKVPFRKKQVSQTKIRVISTILFI	240	
Db	181	KIFCILYAIIFGIFLFGLAGIGDQGTIFGKSIAARVEKVPFRKKQVSQTKIRVISTILFI	240	
QY	241	LACGICVFVTIPAVIFKYEIETGTALESIFVWVYLVLTGGLVFPALQPPFESSOKNTIALEKAEFLRDHVCVS	300	
Db	241	LACGICVFVTIPAVIFKYEIETGTALESIFVWVYLVLTGGLVFPALQPPFESSOKNTIALEKAEFLRDHVCVS	300	
QY	301	WFVILVGLYPAAVLSMIGDMLRVLSKTKKEVGEIKAHAAAEWKNVTAEPRETRRLSV	360	

301 WFWILVGLYFAAFLVSMIGDWRVLSKTKTEVEGEIKAAHAEKANTAEFRTRRLSV 360
361 EIHDKLQRAATISMERRRRLGLDORAHSLDMLSPKRSVFAALDTCGRKASSQESINNR 420
361 EIHDKLQRAATISMERRRRLGLDORAHSLDMLSPKRSVFAALDTCGRKASSQESINNR 420
421 NNLRKGPQLNKGQSGASEDNIIKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 480
421 NNLRKGPQLNKGQSGASEDNIIKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 480
481 LDEEKEBEETKCKNSDNSSTAMLTDCIOQHAELENGMIPTDTKOREPENNSLLED 538
481 LDEEKEBEETKCKNSDNSSTAMLTDCIOQHAELENGMIPTDTKOREPENNSLLED 538

RESULT 2
US-09-949-016-7368
; Sequence 7368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7368
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7368

Query Match 100.0%; Score 2760; DB 4; Length 558;
Best Local Similarity 100.0%; Pred. No. 1.4e-246;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPLYTDFFLSLVAPAAAPVCPKATNGQPPAPPTPTPRLSISSRATVVAARMGTSQ 60
DB 21 MFPLYTDFFLSLVAPAAAPVCPKATNGQPPAPPTPTPRLSISSRATVVAARMGTSQ 80
QY 61 GGLQTVMKWKTVAIFVWVVLVTGGLVFRALDQPPFESSQKNTIALEKAEFLRDHVCVS 120
DB 81 GGLQTVMKWKTVAIFVWVVLVTGGLVFRALDQPPFESSQKNTIALEKAEFLRDHVCVS 140
QY 121 POELETLIQHALDADNAGVSPIGNSSNNSHWDLGSAFFAGTVITIGVNIAPSTEGG 180
DB 141 POELETLIQHALDADNAGVSPIGNSSNNSHWDLGSAFFAGTVITIGVNIAPSTEGG 200
QY 181 KIFCILYALFGLFGLAGIDQGTIFGKSIARVEKVKQVSOTKIRVISTILFI 240
DB 201 KIFCILYALFGLFGLAGIDQGTIFGKSIARVEKVKQVSOTKIRVISTILFI 260
QY 241 LAGCIVFVTPVIFKPIBGTWTALESIFVWVVLVTGGLVFRALDQPPFESSQKNTIALEKAEFLRDHVCVS 300
DB 261 LAGCIVFVTPVIFKPIBGTWTALESIFVWVVLVTGGLVFRALDQPPFESSQKNTIALEKAEFLRDHVCVS 320
QY 301 WFWILVGLYFAAFLVSMIGDWRVLSKTKTEVEGEIKAAHAEKANTAEFRTRRLSV 360
DB 321 WFWILVGLYFAAFLVSMIGDWRVLSKTKTEVEGEIKAAHAEKANTAEFRTRRLSV 380
QY 361 EIHDKLQRAATISMERRRRLGLDORAHSLDMLSPKRSVFAALDTCGRKASSQESINNR 420
DB 381 EIHDKLQRAATISMERRRRLGLDORAHSLDMLSPKRSVFAALDTCGRKASSQESINNR 440

QY 421 NNLRKGPQLNKGQSGASEDNIIKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 480
DB 441 NNLRKGPQLNKGQSGASEDNIIKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 500
QY 481 LDEEKEBEETKCKNSDNSSTAMLTDCIOQHAELENGMIPTDTKOREPENNSLLED 538
DB 501 LDEEKEBEETKCKNSDNSSTAMLTDCIOQHAELENGMIPTDTKOREPENNSLLED 558

RESULT 3
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-236-080-6

Query Match 45.2%; Score 1248.5; DB 3; Length 411;
Best Local Similarity 64.3%; Pred. No. 7e-107;
Matches 247; Conservative 53; Mismatches 67; Indels 17; Gaps 5;

QY 17 AAAPVCPKATNGQPPAPPTPTPRLSISSRATVVA-RMEGTSGGLQTVMKWKTVAI 75
DB 2 AAPDLDPKSA-----AQNSKPLRSFSKPTVLASRVSDS---AINVMKWKTSTI 50
QY 76 FVWVVLVTGGLVFRALDQPPFESSQKNTIALEKAEFLRDHVCVSQPELETLIQHALDAD 135
DB 51 FLVWVLYLIIGAAVFKALEQPOEISORTIVIQKTFIAQHACVNSTELDELIQIVAAI 110
QY 136 NAGVSPIGNSSNNSHWDLGSAFFAGTVITIGVNIAPSTEGGKIFCILYALFGLF 195
DB 111 NAGIIPLGSSNQVSHWDLGSSFFAGTVITIGVNIAPSTEGGKIFCILYALFGLF 170
QY 196 GFLLAGIDQGTIFGKSIARVEKVKQVSOTKIRVISTILFIAGCIVFVTPVIF 255
DB 171 GFLLAGIDQGTIFGKSIARVEKVKQVSOTKIRVISTILFIAGCIVFVTPVIF 230
QY 256 KYIEGWTALESIFVWVVLVTGGLVFRALDQPPFESSQKNTIALEKAEFLRDHVCVSQPELETLIQHALDAD 315
DB 231 KHIEGWSALDAIFVWVVLVTGGLVFRALDQPPFESSQKNTIALEKAEFLRDHVCVSQPELETLIQHALDAD 289
QY 316 SMIGDWRVLSKTKTEVEGEIKAAHAEKANTAEFRTRRLSVIHDKLORAATIRSM 375
DB 290 SMIGDWRVLSKTKTEVEGEIKAAHAEKANTAEFRTRRLSVIHDKLORAATIRSM 346
QY 376 BRRRLGLQRAHSLDMLSPKRSV 399
DB 347 -RRKLSAELAGNHNOELTPCMRTL 369

RESULT 4
US-09-236-080-2
; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

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SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-080-2

Query Match
Best Local Similarity 45.0%; Score 1242.5; DB 3; Length 411;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCQPKSATNGQPPAPPTPTPLRLSSSRATVVA-RMEGTSQGLQTVNMKKTVAI 75
Db 2 AAPDLLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKKTVSTI 50

QY 76 FVVVVVYLVGTGLVFRALQEPFESSOKNTIALEKAEFLRDHVCVSPQELTIOHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAI 110

QY 136 NAGVSPIGNSSNNSSHWDLSGSAFFPAGTIVTTIGYGNIAFSTEGGKIFCIIYAFGPIPLF 195
Db 111 NAGIIPLGNTSNQISHWDLSGSAFFPAGTIVTTIGYGNISPRTEGGKIFCIIYALLGPIPLF 170

QY 196 GFLLAGIGDQGTIFGKSIARVEKVKFRKQVSTQKIRVISTILFILAGCIVFVTIPAVIF 255
Db 171 GFLLAGVGDLGTIFGKGIKVEDTIFKNVSTQKIRIISTITIFILFGCVLFVALPAIIF 230

QY 256 KIEGHTALESIVFVVVTLTTVGFDVAGNAGINREWKYKPLVFWFVLVGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYFVVTITLTIGFDYVAGG-SDIEYLDYFKPVVFWFVLVGLAYFAAVL 289

QY 316 SMIGDWLRVLSKTKKEEVEIKAAHAEKANKVTAEPRETRRLRSVEIHDKLOPAAATIRSM 375
Db 290 SMIGDWLRVLSKTKKEEVEGFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSI--- 346

QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
Db 347 -KKLSAELAGNHQELTFCRRTL 369
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RESULT 5

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US-09-336-643A-83
Sequence 83, Application US/09336643A
Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 411
TYPE: PRT
ORGANISM: H. sapiens
US-09-336-643A-83

Query Match
Best Local Similarity 45.0%; Score 1242.5; DB 3; Length 411;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCQPKSATNGQPPAPPTPTPLRLSSSRATVVA-RMEGTSQGLQTVNMKKTVAI 75
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Db 2 AAPDLLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKKTVSTI 50

QY 76 FVVVVVYLVGTGLVFRALQEPFESSOKNTIALEKAEFLRDHVCVSPQELTIOHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAI 110

QY 136 NAGVSPIGNSSNNSSHWDLSGSAFFPAGTIVTTIGYGNIAFSTEGGKIFCIIYAFGPIPLF 195
Db 111 NAGIIPLGNTSNQISHWDLSGSAFFPAGTIVTTIGYGNISPRTEGGKIFCIIYALLGPIPLF 170

QY 196 GFLLAGIGDQGTIFGKSIARVEKVKFRKQVSTQKIRVISTILFILAGCIVFVTIPAVIF 255
Db 171 GFLLAGVGDLGTIFGKGIKVEDTIFKNVSTQKIRIISTITIFILFGCVLFVALPAIIF 230

QY 256 KIEGHTALESIVFVVVTLTTVGFDVAGNAGINREWKYKPLVFWFVLVGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYFVVTITLTIGFDYVAGG-SDIEYLDYFKPVVFWFVLVGLAYFAAVL 289

QY 316 SMIGDWLRVLSKTKKEEVEIKAAHAEKANKVTAEPRETRRLRSVEIHDKLOPAAATIRSM 375
Db 290 SMIGDWLRVLSKTKKEEVEGFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSI--- 346

QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
Db 347 -KKLSAELAGNHQELTFCRRTL 369

RESULT 6
US-09-144-914-8
Sequence 8, Application US/09144914
Patent No. 6309855
GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234
EARLIER FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: FR 96/01565
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 370
TYPE: PRT
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: TREK-1
US-09-144-914-8

Query Match
Best Local Similarity 44.9%; Score 1238.5; DB 3; Length 370;
Matches 246; Conservative 52; Mismatches 68; Indels 17; Gaps 5;

QY 17 AAAPVCQPKSATNGQPPAPPTPTPLRLSSSRATVVA-RMEGTSQGLQTVNMKKTVAI 75
Db 2 AAPDLLDPKSA-----AONSKPRLSPSTKPTVLASRVESDS---AINVMKKTVSTI 50

QY 76 FVVVVVYLVGTGLVFRALQEPFESSOKNTIALEKAEFLRDHVCVSPQELTIOHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI 110

QY 136 NAGVSPIGNSSNNSSHWDLSGSAFFPAGTIVTTIGYGNIAFSTEGGKIFCIIYAFGPIPLF 195
Db 111 NAGIIPLGNTSNQISHWDLSGSAFFPAGTIVTTIGYGNISPRTEGGKIFCIIYALLGPIPLF 170
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QY 196 GFLLAGIGDQGTIFGKSIARVEKVKQVSTQKIRVISTILFILAGCIVFTTIPAVIF 255
DB 171 GFLLAGVGQDGTIFGKGIKAVEDTFIKNNVSTQKIRIISTIFILFGCVLFVALPAVIF 230
QY 256 KYIEGWTALIESIYFVVVTLTTVGFGDFVAGGNAGINREWKPLVFWFVLGLAYFAAVL 315
DB 231 KHIEGWSALDAIYFVITLTTIGFGDYVAGG-SDIEYDFYKEVWVFWFVLGLAYFAAVL 289
QY 316 SMIGDMLRVLSKTKKEVEGVIKAAHAEWKANVTAEFRETRRLSVIHDKLOAAATIRSM 375
DB 290 SMIGDMLRVLSKTKKEVEGFRAHAAEWNTANVTAEFKETRRLSVIYDFKQRTSV--- 346
QY 376 ERRRLGLDQRAHSLDMLSPKRS 398
DB 347 -KKLSAELAGNHQELTPCWT 368

RESULT 7
US-09-949-016-6913
; Sequence 6913, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6913
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6913

Query Match 29.8%; Score 822.5; DB 4; Length 419;
Best Local Similarity 48.4%; Pred. No. 2e-67;
Matches 164; Conservative 55; Mismatches 87; Indels 33; Gaps 4;

QY 20 PUCPKSATNGQPPAPAPTPTPLSLSSRATTVARMEGTSQGGLOTVMKKTVAIFVVV 79
DB 8 PPARPLQAGSGAGPAG-----RAMRSTTLLALLV 39
QY 80 VVYLVGTGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDADNAGV 139
DB 40 LLLVLSGALVFRALQPFHEQQAQRELGVEVREKFLRAHPCVSDQELGLIKEVADALGGA 99
QY 140 SPIGNSNSSH--WDLGSAFFAGTVITTYGNTIAPSTEGGKIFCILYAIPIGIFLPGF 197
DB 100 DPETNSTSNSSHAWDLGSAFFSGTITTYGYNVALRTDAGRLFCIFVALVIGIFLGI 159
QY 198 LLAGIGDQGTIFGKSIARVEKVKQVSTQKIRVISTILFILAGCIVFTTIPAVIFKY 257
DB 160 LLAGVGDRGLSSLRHGIGHIEAIFLKHVPPPELVRLSAMLFLIGCLLFLVLTPTTFVFCY 219
QY 258 IEGWTALIESIYFVVVTLTTVGFGDFVAGGNAGINREWKPLVFWFVLGLAYFAAVL 317
DB 220 MEDWSKLEAIYFVITLTTVGFGDYVAGADPRQD-SPAYQPLVFWFVLGLAYFASVLT 278
QY 318 IGDWLRVLSKTKKEVEGVIKAAHAEWKANVTAEFRETR 356
DB 279 IGNWLRVSRTRAEWGGLTAQAASWTGTVA--RVTOR 315

RESULT 8
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```
US-09-949-016-7809
; Sequence 7809, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7809
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7809
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Query Match 29.8%; Score 822.5; DB 4; Length 440;
Best Local Similarity 48.4%; Pred. No. 2.1e-67;
Matches 164; Conservative 55; Mismatches 87; Indels 33; Gaps 4;

QY 20 PUCPKSATNGQPPAPAPTPTPLSLSSRATTVARMEGTSQGGLOTVMKKTVAIFVVV 79
DB 29 PPARPLQAGSGAGPAG-----RAMRSTTLLALLV 60
QY 80 VVYLVGTGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDADNAGV 139
DB 61 LLLVLSGALVFRALQPFHEQQAQRELGVEVREKFLRAHPCVSDQELGLIKEVADALGGA 120
QY 140 SPIGNSNSSH--WDLGSAFFAGTVITTYGNTIAPSTEGGKIFCILYAIPIGIFLPGF 197
DB 121 DPETNSTSNSSHAWDLGSAFFSGTITTYGYNVALRTDAGRLFCIFVALVIGIFLGI 180
QY 198 LLAGIGDQGTIFGKSIARVEKVKQVSTQKIRVISTILFILAGCIVFTTIPAVIFKY 257
DB 181 LLAGVGDRGLSSLRHGIGHIEAIFLKHVPPPELVRLSAMLFLIGCLLFLVLTPTTFVFCY 240
QY 258 IEGWTALIESIYFVVVTLTTVGFGDFVAGGNAGINREWKPLVFWFVLGLAYFAAVL 317
DB 241 MEDWSKLEAIYFVITLTTVGFGDYVAGADPRQD-SPAYQPLVFWFVLGLAYFASVLT 299
QY 318 IGDWLRVLSKTKKEVEGVIKAAHAEWKANVTAEFRETR 356
DB 300 IGNWLRVSRTRAEWGGLTAQAASWTGTVA--RVTOR 336
```

```
RESULT 9
US-09-432-470-2
; Sequence 2, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; CURRENT FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 393
; TYPE: PRT
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ORGANISM: HOMO SAPIENS
US-09-432-470-2

Query Match 29.4%; Score 812.5; DB 4; Length 393;
Best Local Similarity 53.8%; Pred. No. 1.5e-66;
Matches 157; Conservative 53; Mismatches 77; Indels 5; Gaps 3;

QY 67 MKWTKVVAIFVVVVVYLVGTGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELFT 126
DB 1 MRSSTLLALLVLLVLSGALVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELGL 60

QY 127 LIQHLDADNAGVSPICGNSNNSH--WDLGSAFFAGTIVITIGVNTAPTEGGKIPC 184
DB 61 LIKEVADALGGGADPETNSTNSHSAWDLGSAFFAGTIVITIGVNTAPTEGGKIPC 120

QY 185 ILYAIFGIFLPGFLAGIDGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGC 244
DB 121 IFYALVGIPLGILLAGVDRGSSLRHGIEHIAFLKWHVPPPELVRVLSAMFLILGC 180

QY 245 IVFVTIPAVIFKIEGWTALSIYFVVVLTGFGDFVAGNAGINREWKPLVWFMI 304
DB 181 LFLVLTPTVFCVMDWSKLEAIFVIVLTGFGDYVAGADPRD-SPAYOPLVWFMI 239

QY 305 LVGLAYFAVLSMIGDLVLSKTKVEGEIKAHAAEWKANVTAEFRTRR 356
DB 240 LGLAYFASVLTITGNLVRVSRTRAEAGLTAQAASWTGTVTA--RVTOR 289

RESULT 10
US-09-432-470-4
Query Match 29.4%; Score 812.5; DB 4; Length 393;
Best Local Similarity 53.8%; Pred. No. 1.5e-66;
Matches 157; Conservative 53; Mismatches 77; Indels 5; Gaps 3;

QY 67 MKWTKVVAIFVVVVVYLVGTGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELFT 126
DB 1 MRSSTLLALLVLLVLSGALVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELGL 60

QY 127 LIQHLDADNAGVSPICGNSNNSH--WDLGSAFFAGTIVITIGVNTAPTEGGKIPC 184
DB 61 LIKEVADALGGGADPETNSTNSHSAWDLGSAFFAGTIVITIGVNTAPTEGGKIPC 120

QY 185 ILYAIFGIFLPGFLAGIDGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGC 244
DB 121 IFYALVGIPLGILLAGVDRGSSLRHGIEHIAFLKWHVPPPELVRVLSAMFLILGC 180

QY 245 IVFVTIPAVIFKIEGWTALSIYFVVVLTGFGDFVAGNAGINREWKPLVWFMI 304
DB 181 LFLVLTPTVFCVMDWSKLEAIFVIVLTGFGDYVAGADPRD-SPAYOPLVWFMI 239

QY 305 LVGLAYFAVLSMIGDLVLSKTKVEGEIKAHAAEWKANVTAEFRTRR 356
DB 240 LGLAYFASVLTITGNLVRVSRTRAEAGLTAQAASWTGTVTA--RVTOR 289

Query Match 29.4%; Score 812.5; DB 4; Length 393;
Best Local Similarity 53.8%; Pred. No. 1.5e-66;
Matches 157; Conservative 53; Mismatches 77; Indels 5; Gaps 3;

QY 67 MKWTKVVAIFVVVVVYLVGTGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELFT 126
DB 1 MRSSTLLALLVLLVLSGALVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELGL 60

QY 127 LIQHLDADNAGVSPICGNSNNSH--WDLGSAFFAGTIVITIGVNTAPTEGGKIPC 184
DB 61 LIKEVADALGGGADPETNSTNSHSAWDLGSAFFAGTIVITIGVNTAPTEGGKIPC 120

QY 185 ILYAIFGIFLPGFLAGIDGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGC 244
DB 121 IFYALVGIPLGILLAGVDRGSSLRHGIEHIAFLKWHVPPPELVRVLSAMFLILGC 180

QY 245 IVFVTIPAVIFKIEGWTALSIYFVVVLTGFGDFVAGNAGINREWKPLVWFMI 304
DB 181 LFLVLTPTVFCVMDWSKLEAIFVIVLTGFGDYVAGADPRD-SPAYOPLVWFMI 239

QY 305 LVGLAYFAVLSMIGDLVLSKTKVEGEIKAHAAEWKANVTAEFRTRR 356
DB 240 LGLAYFASVLTITGNLVRVSRTRAEAGLTAQAASWTGTVTA--RVTOR 289

DB 240 LGLAYFASVLTITGNLVRVSRTRAEAGLTAQAASWTGTVTA--RVTOR 289

RESULT 11
US-09-561-763-2
Query Match 17.5%; Score 483; DB 4; Length 499;
Best Local Similarity 25.8%; Pred. No. 6.9e-36;
Matches 131; Conservative 81; Mismatches 185; Indels 110; Gaps 14;

QY 79 VVVVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELTIQHLDADNAG 138
DB 12 IIFVLAIGAAIFEVLEBPHWEAKGVYTKLHLLKSPFCLGQEGDLKILEVVSAAAGQ 71

QY 139 VSPICGNSNNSHMDLGSAPFAGTIVITIGVNTAPTEGGKIFCILYAIIEGIFLPGFL 198
DB 72 VAITGNQTFN--NMWPNAMIPAAVITIGVNTAPTEGGKIFCILYAIIEGIFLPGFL 126

QY 199 LAGIDQGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGCIVFVTIPAVIFKVI 258
DB 127 LTWI-SALGKFFGGRKALGQPLTKRGVSLRKAQITCTVIFVWGLVHLVIPPVFWMT 185

QY 259 EGWTALESIIYFVVVLTGFGDFVAGNAGINREWKPLVWFVILVGLAYFAVLSMI 318
DB 186 EGWNYIEGLYSPITISTIGFGDFVAGVNPSTANTHALYRYFVELWYLGIA----- 236

QY 319 GDLVLSKTKVEGEIKAHAAEWKANVTAEFRTRRLSVIEIHDKLQRAATIRSMER 378
DB 237 --WLSLF-----VNMKVS-----MFVEVHKAIK-----KRRRR 263

QY 379 RLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNRLK-----CP 428
DB 264 KESPESSPHSRKALQVKGSTASKOVNIFSLSKKEETYNLKIQKKAAMTSGGETCP 323

QY 429 -EQLNKHQOG-----ASEDNINKFGSTSLTKRKNKDLKTLKLPED 468
DB 324 GPGLGPGCGGLPALPPLVPLVYVSKNRVPTLEEVSTQLRSKHGVSRSDEAVARAPED 383

QY 469 VQKIYKTRNYSLEEKKEE-----TERKCNSDNSSTAMLTDC 507
DB 384 SSPAPEFPMN-OLDRISEECBPMDAQDYHPLIFQDASITFVNTAEAGLSDEETSKSLEDN 442

QY 508 I-----QQHAE-----LENGMIPTDTK 524
DB 443 LAGEBSPQGAERAKAPLNWGEFPSSSE 469

Query Match 17.5%; Score 483; DB 4; Length 499;
Best Local Similarity 25.8%; Pred. No. 6.9e-36;
Matches 131; Conservative 81; Mismatches 185; Indels 110; Gaps 14;

QY 79 VVVVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELTIQHLDADNAG 138
DB 12 IIFVLAIGAAIFEVLEBPHWEAKGVYTKLHLLKSPFCLGQEGDLKILEVVSAAAGQ 71

QY 139 VSPICGNSNNSHMDLGSAPFAGTIVITIGVNTAPTEGGKIFCILYAIIEGIFLPGFL 198
DB 72 VAITGNQTFN--NMWPNAMIPAAVITIGVNTAPTEGGKIFCILYAIIEGIFLPGFL 126

QY 199 LAGIDQGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGCIVFVTIPAVIFKVI 258
DB 127 LTWI-SALGKFFGGRKALGQPLTKRGVSLRKAQITCTVIFVWGLVHLVIPPVFWMT 185

QY 259 EGWTALESIIYFVVVLTGFGDFVAGNAGINREWKPLVWFVILVGLAYFAVLSMI 318
DB 186 EGWNYIEGLYSPITISTIGFGDFVAGVNPSTANTHALYRYFVELWYLGIA----- 236

QY 319 GDLVLSKTKVEGEIKAHAAEWKANVTAEFRTRRLSVIEIHDKLQRAATIRSMER 378
DB 237 --WLSLF-----VNMKVS-----MFVEVHKAIK-----KRRRR 263

QY 379 RLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNRLK-----CP 428
DB 264 KESPESSPHSRKALQVKGSTASKOVNIFSLSKKEETYNLKIQKKAAMTSGGETCP 323

QY 429 -EQLNKHQOG-----ASEDNINKFGSTSLTKRKNKDLKTLKLPED 468
DB 324 GPGLGPGCGGLPALPPLVPLVYVSKNRVPTLEEVSTQLRSKHGVSRSDEAVARAPED 383

QY 469 VQKIYKTRNYSLEEKKEE-----TERKCNSDNSSTAMLTDC 507
DB 384 SSPAPEFPMN-OLDRISEECBPMDAQDYHPLIFQDASITFVNTAEAGLSDEETSKSLEDN 442

QY 508 I-----QQHAE-----LENGMIPTDTK 524
DB 443 LAGEBSPQGAERAKAPLNWGEFPSSSE 469

RESULT 12
US-09-431-367B-2
Query Match 29.4%; Score 812.5; DB 4; Length 393;
Best Local Similarity 53.8%; Pred. No. 1.5e-66;
Matches 157; Conservative 53; Mismatches 77; Indels 5; Gaps 3;

QY 67 MKWTKVVAIFVVVVVYLVGTGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELFT 126
DB 1 MRSSTLLALLVLLVLSGALVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELGL 60

QY 127 LIQHLDADNAGVSPICGNSNNSH--WDLGSAFFAGTIVITIGVNTAPTEGGKIPC 184
DB 61 LIKEVADALGGGADPETNSTNSHSAWDLGSAFFAGTIVITIGVNTAPTEGGKIPC 120

QY 185 ILYAIFGIFLPGFLAGIDGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGC 244
DB 121 IFYALVGIPLGILLAGVDRGSSLRHGIEHIAFLKWHVPPPELVRVLSAMFLILGC 180

QY 245 IVFVTIPAVIFKIEGWTALSIYFVVVLTGFGDFVAGNAGINREWKPLVWFMI 304
DB 181 LFLVLTPTVFCVMDWSKLEAIFVIVLTGFGDYVAGADPRD-SPAYOPLVWFMI 239

QY 305 LVGLAYFAVLSMIGDLVLSKTKVEGEIKAHAAEWKANVTAEFRTRR 356
DB 240 LGLAYFASVLTITGNLVRVSRTRAEAGLTAQAASWTGTVTA--RVTOR 289

ORGANISM: HOMO SAPIENS
US-09-431-367B-2
Query Match 29.4%; Score 812.5; DB 4; Length 393;
Best Local Similarity 53.8%; Pred. No. 1.5e-66;
Matches 157; Conservative 53; Mismatches 77; Indels 5; Gaps 3;

QY 67 MKWTKVVAIFVVVVVYLVGTGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELFT 126
DB 1 MRSSTLLALLVLLVLSGALVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELGL 60

QY 127 LIQHLDADNAGVSPICGNSNNSH--WDLGSAFFAGTIVITIGVNTAPTEGGKIPC 184
DB 61 LIKEVADALGGGADPETNSTNSHSAWDLGSAFFAGTIVITIGVNTAPTEGGKIPC 120

QY 185 ILYAIFGIFLPGFLAGIDGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGC 244
DB 121 IFYALVGIPLGILLAGVDRGSSLRHGIEHIAFLKWHVPPPELVRVLSAMFLILGC 180

QY 245 IVFVTIPAVIFKIEGWTALSIYFVVVLTGFGDFVAGNAGINREWKPLVWFMI 304
DB 181 LFLVLTPTVFCVMDWSKLEAIFVIVLTGFGDYVAGADPRD-SPAYOPLVWFMI 239

QY 305 LVGLAYFAVLSMIGDLVLSKTKVEGEIKAHAAEWKANVTAEFRTRR 356
DB 240 LGLAYFASVLTITGNLVRVSRTRAEAGLTAQAASWTGTVTA--RVTOR 289

FILE REFERENCE: MNI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 2
LENGTH: 499
TYPE: PRT
ORGANISM: Homo sapiens
US-09-431-367B-2

Query Match 17.5%; Score 483; DB 4; Length 499;
Best Local Similarity 25.8%; Pred. No. 6.9e-36;
Matches 131; Conservative 81; Mismatches 185; Indels 110; Gaps 14;
QY 79 VVYLVTGVLVFRALQPESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDADNAG 138
DB 12 IIFYLGAIAAIFVLEPHWKEAKQNYTKLHLLKEFPCLQGQGLDKILEVVSDAAGQ 71
QY 139 VSPIGNSSNHHWDLGSAFFPAGTIVTTIGYGNIAAPSTEGGKIPCLYAIAGIFPLGFL 198
DB 72 VALTGNQTFN--NWNPNAMIFAAVTTTIGYGNVAPKTPAGRLFCVFFGLGVPL---C 126
QY 199 LAGIGDQGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPAVIFKYI 258
DB 127 LTWI-SALGKFFGGRAKRLGQPLTKRGVSLRKAQITCTWIFVWGLVHLVIPPVPMVT 185
QY 259 EGTWALIESYFVVVTTTGGDFVAGNAGINREWYKPLVFWFWLVLGLAYFAAVLSMI 318
DB 186 EGNYYIEGLYSPITITISITIGDFVAGVNPNSANYHALYRYFVVELWYLGLA----- 236
QY 319 GDLRLVLSKTKKEVGEIKAHAAEWKANYTAEPRETRRLSVEIHDKLRQAAATIRSMERR 378
DB 237 --WLSLF-----VNWKVS-----NFVEVHKAIK-----KRRRR 263
QY 379 RLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNRLK-----GP 428
DB 264 KESFESSPHSRKALQVKGSTASKDVNIFSLSKETYNLDLIQICKAMKTSGGGETGP 323
QY 429 -EOLNKHGQ-----ASENIINKGSTSLRTRKKNKOLKLTLPED 468
DB 324 GFLGPGQGGPLPALPFLVPLVYVKNRVTLEEVSTLRSKHGVSRSPPDEAVARAPED 383
QY 469 VQIKYKTFNYSLEDEKKEB-----TEKMCNSDMSSTAMLTDC 507
DB 384 SSPAPEVFMN-QLDRISBCEPDAQDYHPLIFQDASITFVWTEAGLSDEETSLSLEDN 442
QY 508 I-----QCHAE-----LENGMIPTDK 524
DB 443 LAGEESPQGAEAAPLNMGEPPSSSE 469

RESULT 13
US-09-236-080-4
Sequence 4, Application US/09236080
Patent No. 6242217
GENERAL INFORMATION:
APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-080-4

Query Match 16.2%; Score 447; DB 3; Length 107;
Best Local Similarity 77.6%; Pred. No. 1.3e-33;
Matches 83; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
QY 144 NSSNNSSHHWDLGSAFFPAGTIVTTIGYGNIAAPSTEGGKIPCLYAIAGIFPLGFLAGIG 203
DB 1 NSSNQVSHWDLGSSFFPAGTIVTTIGFNGNISRTGEGKIPCIYIALLGILPLGFLAGVG 60
QY 204 DOLGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTI 250
DB 61 DOLGTIFGKIAKVEDTIFKNVSTKIRIISTIFILGCVLFVAL 107

RESULT 14
US-08-749-816-2
Sequence 2, Application US/08749816
Patent No. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemare, Eric
APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazdunki, Michel
APPLICANT: Roney, Georges
APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989.6351P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-816-2

Query Match 14.6%; Score 403; DB 3; Length 336;
Best Local Similarity 33.2%; Pred. No. 9.4e-29;
Matches 95; Conservative 53; Mismatches 104; Indels 34; Gaps 9;
QY 76 FVVV--VVYLVTVGLVFRALQPESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALD 133
DB 25 FLVLYLVTVGLVFRALQPESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALD 84
QY 134 ADNAGVSPIGNSSNHHWDLGSAFFPAGTIVTTIGYGNIAAPSTEGGKIPCLYAIAGIFGIP 193
DB 85 ASNYGVSVLSNAGN-WNWDFTSALFFASTVLTSTTGHTVPLSDGKAPCIYIVGIP 143
QY 194 LFGFLAGIGDQGTIFGKSIARVEKVRKQV-----SQTIRVISTIL---PILA 242

Db 144 FTLLFTAV-----VQRITVHTRRPVLYPHIRWGFSKQVVAIVHAVLLGFVT 192
QY 243 GCIVFTIPAVIFKYE-GWTALESYFVVVTLTTVGFGDFVAGNAGINRYREWKPLVW 301
Db 193 SCFFP--IPAAVSVLEDDNLFESYFCFISLSTIGLDYVPGEGYNQKRELYKIGIT 250
QY 302 FWILVGLAYFAAVLSMIGDMLRVLSK-----KTKEEVGEIKAHAAE 342
Db 251 CYLLGLGLIAMLVVLETCF-LHELKPKRMFYVKKDKDEQVHIIE 295

RESULT 15

US-09-144-914-2
; Sequence 2, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TWIK-1
US-09-144-914-2

Query Match 14.6%; Score 403; DB 3; Length 336;
Best Local Similarity 33.2%; Pred. No. 9.4e-29;
Matches 95; Conservative 53; Mismatches 104; Indels 34; Gaps 9;
QY 76 FVVV--VYLVTCGLVFRALQPFESSQKNTIALEKAEFLRDHVCVSPQETLIQHLD 133
Db 25 FLVIGVLLYLVFGAVFSSVELPYEDLLROELKRLKRFLEEHECLSEQQLEQFLGRVLE 84
QY 134 ADNAGVSPIGNSNNSHWDLSAFAFFAGTVITIGYNIAPSTEGGKIPFCILYAFGIP 193
Db 85 ASNYGVSVLSNAGN-KNWDFTSALFASVLTSTGTGHTVPLSDGGKAFCIYVIGIP 143
QY 194 LFGFLAGIGDQGTIGKSIARVEKVKRQV-----SOTKIRVISTIL--FILA 242
Db 144 FTLLFTAV-----VQRITVHTRRPVLYPHIRWGFSKQVVAIVHAVLLGFVT 192
QY 243 GCIVFTIPAVIFKYE-GWTALESYFVVVTLTTVGFGDFVAGNAGINRYREWKPLVW 301
Db 193 SCFFP--IPAAVSVLEDDNLFESYFCFISLSTIGLDYVPGEGYNQKRELYKIGIT 250
QY 302 FWILVGLAYFAAVLSMIGDMLRVLSK-----KTKEEVGEIKAHAAE 342
Db 251 CYLLGLGLIAMLVVLETCF-LHELKPKRMFYVKKDKDEQVHIIE 295

Search completed: April 28, 2005, 13:26:50
Job time : 45 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2760	100.0		538	5	AAB47930	Human TRE3
2	2760	100.0		538	5	AAE16596	Human TWI
3	2760	100.0		538	5	ABP69333	Human pol
4	2697	97.7		543	5	AAE21804	Human TRE
5	2697	97.7		543	5	AAU81354	Human TRE
6	2697	97.7		543	5	AAU79472	Human nov
7	2697	97.7		543	5	AAU79472	Human nov
8	2697	97.7		543	6	AB883542	Hypothala
9	2697	97.7		543	6	ADA05746	Human NOV
10	2697	97.7		543	8	ADN08315	Novel pro
11	2693	97.6		543	5	AAU79473	Human NOV
12	2657.5	96.3		724	5	AAO14193	Human nov
13	1630	59.1		383	4	ABG02731	Human tra
14	1412.5	51.2		557	4	ABG08305	Novel hum
15	1251.5	45.3		411	3	AAE10342	Novel hum
16	1251.5	45.3		422	7	ADP033575	Murine TR
17	1248.5	45.2		411	2	ADP033575	Human GPC
18	1247.5	45.2		370	2	AAU28497	Human GPC
19	1243	45.0		411	3	AAE10341	Mouse h-T
20	1242.5	45.0		411	3	AAE10341	Ay30648 A mechani
21	1242.5	45.0		411	2	AAU34133	Human TRE
22	1242.5	45.0		411	2	AAU28496	Human pot
23	1242.5	45.0		411	4	AAE50044	h-TREK1 p
24	1242.5	45.0		411	7	ADP033586	Human TRE
25	1242.5	45.0		411	8	ADQ76698	Human GPC
26	1235	44.7		411	5	AAE16597	Human tw
27	1235	44.7		411	5	AAE16597	Human TWI

XX PS Claim 3; Page 44-46; 50pp; English.

XX CC This sequence shows a protein, which constitutes a human K⁺ channel, TREK2, which has two pore domains that produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K⁺ conditions. TREK2 is activated by general anaesthetics at clinical concentrations. It is modulated by different types of neurotransmitter receptors. The TREK2 gene produces a cDNA of 2730 bp which contains an open reading frame of 1617 nucleotides. The TREK2 protein has the same overall structure as previously described K⁺ channels. It has four membrane spanning domains (M1-M4), two pore domains (P1-P2) and an extended loop between M1 and P1. TREK2 shares 63% identity and 78% homology to TREK1. The chromosomal location of the TREK2 gene is 14q31.1. TREK2 is useful in methods for screening various compounds. In particular, the protein is useful in methods for identifying biologically active compounds with anaesthetic properties

XX SQ Sequence 538 AA;

Query Match 100.0%; Score 2760; DB 5; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.7e-244;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPLYTDFLSLVAVPAAAPVCPKSAATNGQPAPAPTPTPLSISSRATVVARMEGTSQ 60
 DB 1 MFPLYTDFLSLVAVPAAAPVCPKSAATNGQPAPAPTPTPLSISSRATVVARMEGTSQ 60

QY 61 GGLQTMKWKTTVAIFVWVYLVVTGGLVFRALBOPFESSQKNTALEKAEFLRDHVCVS 120
 DB 61 GGLQTMKWKTTVAIFVWVYLVVTGGLVFRALBOPFESSQKNTALEKAEFLRDHVCVS 120

QY 121 POELETLIQHALDADNAGVSPICGNSNNSHWDLSGAFPAFTVITTYGNIAPSTEGG 180
 DB 121 POELETLIQHALDADNAGVSPICGNSNNSHWDLSGAFPAFTVITTYGNIAPSTEGG 180

QY 181 KIFCILYALFGLPFLGAGDQGLGTIFGKSIARVEKVFRRKQVSOQTKIRVISTILFI 240
 DB 181 KIFCILYALFGLPFLGAGDQGLGTIFGKSIARVEKVFRRKQVSOQTKIRVISTILFI 240

QY 241 LAGCIVFTVPIAVIPKYGWTALESYFVWVLTGTFGDFVAGNAGINREMYKPLV 300
 DB 241 LAGCIVFTVPIAVIPKYGWTALESYFVWVLTGTFGDFVAGNAGINREMYKPLV 300

QY 301 WFWILVGLAYFAVLISMGDLRVLSKTKVEEVEIKAAAEWKANVTAEFRETRELVS 360
 DB 301 WFWILVGLAYFAVLISMGDLRVLSKTKVEEVEIKAAAEWKANVTAEFRETRELVS 360

QY 361 EIHDKLQRAATIRSMERRLGLDQRAHSLDMLSPKRSVFAALDTCGRFKASSQESINNRP 420
 DB 361 EIHDKLQRAATIRSMERRLGLDQRAHSLDMLSPKRSVFAALDTCGRFKASSQESINNRP 420

QY 421 NNLRKGPQLNKGCGASEDNIINFGSTSLTKRNKDLKKTLPEDVOKYKTPRNTS 480
 DB 421 NNLRKGPQLNKGCGASEDNIINFGSTSLTKRNKDLKKTLPEDVOKYKTPRNTS 480

QY 481 LDEEKKKEETKNCNSDSTAMLTDICIQHAELENGMIPTDKREPENNILLDRN 538
 DB 481 LDEEKKKEETKNCNSDSTAMLTDICIQHAELENGMIPTDKREPENNILLDRN 538

RESULT 2
 AAE16596
 ID AAE16596 standard; protein; 538 AA.
 XX AAE16596;
 AC AAE16596;
 XX 18-APR-2002 (first entry)
 XX Human TWIK-Related K⁺ channel-2 (TREK-2) protein.
 DE Human; TWIK-Related K⁺ Channel-2; TREK-2; anaesthetic; chromosome 14q31;
 KW screening.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 72..90

FT Domain /note= "M1 membrane spanning segment"

FT Domain 152..175

FT Domain /note= "p1 pore domain"

FT Region 183..203

FT Region /note= "M2 membrane spanning segment"

FT Region 234..255

FT Region /note= "M3 membrane spanning segment"

FT Domain 261..284

FT Domain /note= "p2 pore domain"

FT Region 300..319

FT Region /note= "M4 membrane spanning segment"

XX WO200200715-A2.

XX 03-JAN-2002.

XX 27-JUN-2001; 2001WO-IB001436.

XX 27-JUN-2000; 2000US-0214559P.

XX 27-JUN-2001; 2001US-00892360.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Romey G;

XX WPI; 2002-139903/18.

XX N-PSDB; AAD27459.

XX New mammalian K⁺ channel protein with two pore domains, for screening various compounds, particularly for identifying biologically active compounds with anaesthetic properties.

XX Claim 3; Page 45-47; 50pp; English.

XX The invention relates to a mammalian K⁺ channel protein with two pore domains, called TREK2 (TWIK-Related K⁺ Channel). The protein produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K⁺ conditions. TREK2 is a member of the fatty acid-activated and mechanosensitive K⁺ channel family. TREK-2 gene located on chromosome 14q31 is abundantly expressed in kidney, pancreas and moderately in testis, brain, colon and small intestine. The mammalian K⁺ channel protein is useful in methods for screening various compounds. In particular, the protein is useful in methods for identifying biologically active compounds with anaesthetic properties. The present sequence is human TREK-2 protein

XX SQ Sequence 538 AA;

Query Match 100.0%; Score 2760; DB 5; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.7e-244;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPLYTDFLSLVAVPAAAPVCPKSAATNGQPAPAPTPTPLSISSRATVVARMEGTSQ 60
 DB 1 MFPLYTDFLSLVAVPAAAPVCPKSAATNGQPAPAPTPTPLSISSRATVVARMEGTSQ 60

QY 61 GGLQTMKWKTTVAIFVWVYLVVTGGLVFRALBOPFESSQKNTALEKAEFLRDHVCVS 120
 DB 61 GGLQTMKWKTTVAIFVWVYLVVTGGLVFRALBOPFESSQKNTALEKAEFLRDHVCVS 120

QY 121 POELETLIQHALDADNAGVSPICGNSNNSHWDLSGAFPAFTVITTYGNIAPSTEGG 180
 DB 121 POELETLIQHALDADNAGVSPICGNSNNSHWDLSGAFPAFTVITTYGNIAPSTEGG 180

QY 181 KIFCILYALFGLPFLGAGDQGLGTIFGKSIARVEKVFRRKQVSOQTKIRVISTILFI 240
 DB 181 KIFCILYALFGLPFLGAGDQGLGTIFGKSIARVEKVFRRKQVSOQTKIRVISTILFI 240

QY 241 LAGCIVFTIPAVIPKIVGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLV 300
 DB 241 LAGCIVFTIPAVIPKIVGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLV 300
 QY 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAFRETRRLSV 360
 DB 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAFRETRRLSV 360
 QY 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
 DB 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
 QY 421 NNLRKGPQLNKGQAGASEDNIIINFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYS 480
 DB 421 NNLRKGPQLNKGQAGASEDNIIINFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYS 480
 QY 481 LDEKKKEETKMCNSDNSSTAMLTDCIQOHALENGMIPTDTKDREPNNSLLEDNRN 538
 DB 481 LDEKKKEETKMCNSDNSSTAMLTDCIQOHALENGMIPTDTKDREPNNSLLEDNRN 538
 RESULT 3
 ABP69333
 ID ABP69333 standard; protein; 538 AA.
 XX AC ABP69333;
 XX DT 20-JAN-2003 (first entry)
 XX DE Human polypeptide SEQ ID NO 1380.
 XX KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cystostatic; immunomodulator; nootropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
 KW antiarthritic.
 OS Homo sapiens.
 XX WO200270539-A2.
 XX PD 12-SEP-2002.
 XX PP 05-MAR-2002; 2002WO-US005095.
 XX PR 05-MAR-2001; 2001US-00799451.
 XX PA (HYSEQ-) HYSEQ INC.
 XX PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao Q, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 DR WPI; 2002-759812/82.
 DR N-PSDB; ABZ11550.
 XX PT New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.
 XX PS Claim 9; SEQ ID NO 1380; 1012pp + Sequence Listing; English.
 XX CC The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
 CC ABZ12066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical

CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 538 AA;
 SQ
 Query Match 100.0%; Score 2760; DB 5; Length 538;
 Best Local Similarity 100.0%; Pred No. 1.7e-244; Indels 0; Gaps 0;
 Matches 538; Conservative 0; Mismatches 0;
 QY 1 MFPLYTDFFLSLVAVPAAAPVCPKSAATNGQPAPPTPRLSSSRATVVARMEGTSQ 60
 DB 1 MFPLYTDFFLSLVAVPAAAPVCPKSAATNGQPAPPTPRLSSSRATVVARMEGTSQ 60
 QY 61 GGLQTVMEKTKTVAFVAVVAVVYLVVTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVS 120
 DB 61 GGLQTVMEKTKTVAFVAVVAVVYLVVTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVS 120
 QY 121 POELETLLIOHALDADNAGVSPIGNSSNNSSHWDLSAPFAAGTAVTTIGYGNIAPESTEG 180
 DB 121 POELETLLIOHALDADNAGVSPIGNSSNNSSHWDLSAPFAAGTAVTTIGYGNIAPESTEG 180
 QY 181 KIFCILYAFIGPLFGFLLAGIGDQGTIFGKSIARVEKVFRRKQVSOVKIRVISTILFI 240
 DB 181 KIFCILYAFIGPLFGFLLAGIGDQGTIFGKSIARVEKVFRRKQVSOVKIRVISTILFI 240
 QY 241 LAGCIVFTIPAVIPKIVGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLV 300
 DB 241 LAGCIVFTIPAVIPKIVGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLV 300
 QY 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAFRETRRLSV 360
 DB 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAFRETRRLSV 360
 QY 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
 DB 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
 QY 421 NNLRKGPQLNKGQAGASEDNIIINFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYS 480
 DB 421 NNLRKGPQLNKGQAGASEDNIIINFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYS 480
 QY 481 LDEKKKEETKMCNSDNSSTAMLTDCIQOHALENGMIPTDTKDREPNNSLLEDNRN 538
 DB 481 LDEKKKEETKMCNSDNSSTAMLTDCIQOHALENGMIPTDTKDREPNNSLLEDNRN 538
 RESULT 4
 AAEE21804
 ID AAEE21804 standard; protein; 543 AA.
 XX AC AAEE21804;
 XX DT 16-JUL-2002 (first entry)
 XX DE Human TREK2 protein.
 XX KW Human; hTREK2 protein; cancer; diabetes; pulmonary disease; asthma;
 KW cardiovascular disease; inflammatory disease; psychiatric disorder;
 KW renal disease; neurodegenerative disease; neurological disorder;
 KW Alzheimer's disease; depression; schizophrenia; stroke; vaccine; trauma;
 XX pain.
 OS Homo sapiens.
 XX GB2365010-A.
 XX

PD 13-FEB-2002.
XX
PF 24-APR-2001; 2001GB-00010129.
XX
PR 25-APR-2000; 2000GB-00010060.
PR 01-JUN-2000; 2000GB-00013370.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Chapman CG, Duckworth DM;
XX
XX WPI; 2002-332557/37.
DR N-PSDB; AAD34451.
XX
XX Novel human TREK2 (HTREK2) polypeptide and polynucleotide encoding it,
PT useful for identifying agonists and antagonists in the treatment of
PT diseases associated with a HTREK2 imbalance, such as diabetes, cancers or
PT asthma.
XX
XX Claim 1; Page 21-22; 29pp; English.
XX
XX The invention relates to human HTREK2 polypeptides and nucleic acid
CC molecules encoding such polypeptides. TREK2 polypeptides are useful in
CC screening assays to identify compounds that may stimulate or inhibit
CC their function or level of expression. Sequences of the invention are
CC used to treat cancer, diabetes, asthma, pulmonary disease, cardiovascular
CC diseases, inflammatory disease, renal disease, pain, psychiatric
CC disorders including depression and schizophrenia, neurodegenerative
CC disease including Alzheimer's disease, stroke and head trauma and
CC neurological disorders. They are also used as vaccines. The present
CC sequence is human HTREK2 protein
XX
SQ Sequence 543 AA;

Query Match 97.7%; Score 2697; DB 5; Length 543;
Best Local Similarity 100.0%; Pred. No. 1.1e-238;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATGPPAPPTPTPLSLSSRATVVARMEGTSQGLQTVMKWKT 72
DB 18 VAVPAAAPVCPKSAATGPPAPPTPTPLSLSSRATVVARMEGTSQGLQTVMKWKT 77

QY 73 VAIFVVVVVLTGVLFRALQEPSSQKNTIALEKAEFLRDHVCVSPQELTLIQHAL 132
DB 78 VAIFVVVVVLTGVLFRALQEPSSQKNTIALEKAEFLRDHVCVSPQELTLIQHAL 137

QY 133 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTIVTTTGYGNIAPSTGGKIFCLLYAIFGI 192
DB 138 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTIVTTTGYGNIAPSTGGKIFCLLYAIFGI 197

QY 193 PLFGFLLAGIDGLGTFGKSTARVEKVRKKQVSTKIRVSTILFILAGCIVFTTIPA 252
DB 198 PLFGFLLAGIDGLGTFGKSTARVEKVRKKQVSTKIRVSTILFILAGCIVFTTIPA 257

QY 253 VIFKYIEGTALIESIYFVVVLTGTFGDFVAGNAGINRYREWKPLVFWFVLVGLAYFA 312
DB 258 VIFKYIEGTALIESIYFVVVLTGTFGDFVAGNAGINRYREWKPLVFWFVLVGLAYFA 317

QY 313 AVLSMIGDWLRLVSKTKKEVGBIKAHAAEWKANVTABPRTTRRLSVSEIHDKLQAAAT 372
DB 318 AVLSMIGDWLRLVSKTKKEVGBIKAHAAEWKANVTABPRTTRRLSVSEIHDKLQAAAT 377

QY 373 RSMERRRLGIDRAHSLDMLSPKRSVFAALDTGRFKASSQSINNNRNPNRLKGPQLN 432
DB 378 RSMERRRLGIDRAHSLDMLSPKRSVFAALDTGRFKASSQSINNNRNPNRLKGPQLN 437

QY 433 KHGQGAASEDNIINKFSTSRLLTKRKNKDLKLTLPEDVQKIYKTFRNYSLDEKKEBETEK 492
DB 438 KHGQGAASEDNIINKFSTSRLLTKRKNKDLKLTLPEDVQKIYKTFRNYSLDEKKEBETEK 497

QY 493 MCNSDSSSTAMLTDCITQOHAELNGMIPDTDKREPENNSLLEDNRN 543
|||||

DB 498 MCNSDSSSTAMLTDCITQOHAELNGMIPDTDKREPENNSLLEDNRN 543

RESULT 5
AAU81354
ID AAU81354 standard; protein; 543 AA.
XX
XX AAU81354;
XX
XX 09-APR-2002 (first entry)
XX
XX Novel human ion channel protein #34.
DE XX
XX Human; ion channel; anti-HIV; analgesic; cytostatic; antidiabetic;
KW anorectic; metabolic; hypertensive; hypotensive; thrombolytic; cardiac;
KW antiatherosclerotic; neuroleptic; antimigraine; antiparkinsonian;
KW tranquiliser; antidepressant; neuroprotective; anticonvulsant; pain;
KW antinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antipsoriatic; antiasthmatic; vulnary; asthmic; traumatic brain injury;
KW psychiatric disorder; gene therapy; asthma; cancer; diabetes; anorexia;
KW human immunodeficiency virus; HIV-1; HIV-2; cancer; diabetes; anorexia;
KW myocardial infarction; Parkinson's disease; schizophrenia; anxiety;
KW dementia; Huntington's disease; thyroid disorder; inflammation;
KW autoimmune disorder; hormonal disorder; renal failure; psoriasis;
KW movement disorder.
XX
XX Homo sapiens.
XX
XX WO200185788-A2.
XX
XX 15-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-US014965.
XX
XX 10-MAY-2000; 2000US-0203305P.
XX 23-MAY-2000; 2000US-0206526P.
XX 25-MAY-2000; 2000US-0207033P.
XX 25-MAY-2000; 2000US-0207092P.
XX 25-MAY-2000; 2000US-0207093P.
XX 07-JUL-2000; 2000US-0216893P.
XX 04-AUG-2000; 2000US-0223245P.
XX 04-OCT-2000; 2000US-0237873P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Roberts SL, Benjamin CW, Karnovsky AM, Ruble CL;
PI
XX
XX WPI; 2002-062237/08.
DR N-PSDB; ABK27503.
XX
XX New polynucleotides, useful for identifying ion channel activity
PT modulators that are used for treating Parkinson's disease, schizophrenia,
PT migraine, anxiety, manic depression, encodes the ion channel polypeptide.
XX
XX Claim 2; Page 89; 172pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) which
CC encodes a novel ion channel protein, ion-x (II). The nucleic acid,
CC protein and antibody are useful for identifying a compound which binds a
CC nucleic acid molecule encoding ion-x. These are useful for treatment of a
CC neurological or psychiatric disorder which modulates ligand binding to
CC ion-x in neurons of the mammal; in gene therapy to restore ion-x activity
CC in certain disease states; for treating asthma, traumatic brain injury,
CC etc; modulators of ion-x activity or expression are useful for treating
CC diseases such as viral infections caused by human immunodeficiency virus
CC (HIV)-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia,
CC hypertension, atherosclerosis, thrombosis, myocardial infarction,
CC cardiomyopathies, anticonvulsants, Parkinson's disease, schizophrenia,
CC migraine, anxiety, manic depression, dementia, Huntington's disease,
CC thyroid disorders, inflammatory conditions, rheumatoid arthritis, and
CC autoimmune disorders, hormonal disorders, renal failure, psoriasis, and
CC movement disorders. AAU81321-AAU81360 represent human ion channel protein
CC sequences of the invention

```

XX  Sequence 543 AA;
SQ
Query Match          97.7%; Score 2697; DB 5; Length 543;
Best Local Similarity 100.0%; Pred. No. 1.1e-238;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATNGQPPAPAPPTPTPLRSLSSRATVVARMEGTSQGLQTVMKWKTIV 72
DB 18 VAVPAAAPVCPKSAATNGQPPAPAPPTPTPLRSLSSRATVVARMEGTSQGLQTVMKWKTIV 77
QY 73 VAIFVVVVVLTGVLFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132
DB 78 VAIFVVVVVLTGVLFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137
QY 133 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTIVTIGYGNIAAPSTEGGKIFCILVAIFGI 192
DB 138 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTIVTIGYGNIAAPSTEGGKIFCILVAIFGI 197
QY 193 PLFGFLLAGIGDQLTIFGKSIARVEKVRKQVQSKIRVISTILFILAGCIVFTTIPA 252
DB 198 PLFGFLLAGIGDQLTIFGKSIARVEKVRKQVQSKIRVISTILFILAGCIVFTTIPA 257
QY 253 VIPKYIEGWTALSIYFVVVLTGVLFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 312
DB 258 VIPKYIEGWTALSIYFVVVLTGVLFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 317
QY 313 AVLSMIGDNLRLVLSKTKKEVGEIKAAHAEKAWKANTVAFRETRRLSVEIHDKLQRAATI 372
DB 318 AVLSMIGDNLRLVLSKTKKEVGEIKAAHAEKAWKANTVAFRETRRLSVEIHDKLQRAATI 377
QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQSSINNRPNRLKGPQQLN 432
DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQSSINNRPNRLKGPQQLN 437
QY 433 KHGQASDNIINKGTSRLTKRQKDKLKTLPEDVQKIYKTFPNYSLDEKKEETEK 492
DB 438 KHGQASDNIINKGTSRLTKRQKDKLKTLPEDVQKIYKTFPNYSLDEKKEETEK 497
QY 493 MCNSDNSSTAMLTDCIQHAELENGMIPTDQKREPNNLSLEDNRN 538
DB 498 MCNSDNSSTAMLTDCIQHAELENGMIPTDQKREPNNLSLEDNRN 543

RESULT 6
AAU79472
ID AAU79472 standard; protein; 543 AA.
XX
XX AC AAU79472;
XX
XX 15-JUL-2002 (first entry)
XX
XX DE Human novel transporter protein.
XX
XX KW Human; transporter; transgenic; transporter mediated disease;
XX KW drug screening; pharmacogenomic analysis; chromosome 18.
XX
XX OS Homo sapiens.
XX
XX PN WO200224748-A2.
XX
XX PD 28-MAR-2002.
XX
XX PF 19-SEP-2001; 2001WO-US029211.
XX
XX PR 19-SEP-2000; 2000US-0233663P.
XX PR 06-DEC-2000; 2000US-00729920.
XX
XX PA (PEKE ) PE CORP NY.
XX
XX PI Guegler K, Ketchum KA, Di Francesco V, Beasley EM;
XX
XX WPI; 2002-351999/38.

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DR N-PSDB; ABK49585, ABK49586.

XX New human transporter proteins and nucleic acids, useful as models in the development of human therapeutic agents, in identifying therapeutic proteins, or as query sequence in database searches to identify related sequences.

XX Claim 1; Fig 2; 207pp; English.

XX The invention relates to a new isolated peptide being a human transporter protein, an allelic variant, orthologue, fragment or sequence that is 70% homologous to the transporter. Also included are a nucleic acid encoding the transporter (including allelic variants, orthologue, fragment or complement), an antibody against the protein, a gene chip comprising the nucleic acids, a transgenic non-human animal comprising the nucleic acids, a nucleic acid vector comprising the nucleic acids, a host cell containing the vector, identifying agents that bind to and/or modulate the function of the transporter, and treating a disease or condition mediated by a human transporter protein by administering to the patient an identified agent or modulator. The peptide sequences and the nucleic acid sequences encoding these peptides can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate transporter activity in cells and tissues that express the transporter. These sequences may also be used as query sequence in database searches to identify other family members or related sequences. The proteins may be used to raise antibodies or to elicit immune response; as a reagent in assays designed to quantitatively determine protein levels in biological fluids; as markers for tissues in which the corresponding protein is expressed; in drug screening assays in cell-based or cell-free systems; to identify compounds that modulate transporter activity of the protein in its natural state or altered form that causes a specific disease or pathology associated with the transporter; as target for diagnosing a disease or predisposition to disease mediated by the peptide; and in pharmacogenomic analysis. The nucleic acids are useful as hybridisation probes or primers; in monitoring the effectiveness of modulating compounds on the expression or activity of the transporter gene in clinical trials or treatment regimen; in diagnostic assays for qualitative changes in transporter nucleic acid expression; and as antisense constructs. The gene for the transporter is located on chromosome 18. The present sequence represents the novel human transporter

Sequence 543 AA;

Query Match 97.7%; Score 2697; DB 5; Length 543;
Best Local Similarity 100.0%; Pred. No. 1.1e-238;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 13 VAVPAAAPVCPKSAATNGQPPAPAPPTPTPLRSLSSRATVVARMEGTSQGLQTVMKWKTIV 72
DB 18 VAVPAAAPVCPKSAATNGQPPAPAPPTPTPLRSLSSRATVVARMEGTSQGLQTVMKWKTIV 77
QY 73 VAIFVVVVVLTGVLFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132
DB 78 VAIFVVVVVLTGVLFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137
QY 133 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTIVTIGYGNIAAPSTEGGKIFCILVAIFGI 192
DB 138 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTIVTIGYGNIAAPSTEGGKIFCILVAIFGI 197
QY 193 PLFGFLLAGIGDQLTIFGKSIARVEKVRKQVQSKIRVISTILFILAGCIVFTTIPA 252
DB 198 PLFGFLLAGIGDQLTIFGKSIARVEKVRKQVQSKIRVISTILFILAGCIVFTTIPA 257
QY 253 VIPKYIEGWTALSIYFVVVLTGVLFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 312
DB 258 VIPKYIEGWTALSIYFVVVLTGVLFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 317
QY 313 AVLSMIGDNLRLVLSKTKKEVGEIKAAHAEKAWKANTVAFRETRRLSVEIHDKLQRAATI 372
DB 318 AVLSMIGDNLRLVLSKTKKEVGEIKAAHAEKAWKANTVAFRETRRLSVEIHDKLQRAATI 377

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QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRNNRLKGPQLN 432
 DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRNNRLKGPQLN 437
 QY 433 KHGQASDNIINKFGSTSRITKRNKDKKTLPEDEVQKIYKTFPNYSIDREKKEETEK 492
 DB 438 KHGQASDNIINKFGSTSRITKRNKDKKTLPEDEVQKIYKTFPNYSIDREKKEETEK 497
 QY 493 MCNSDNSSTAMLTDCIQOHAELNGMIPTDTKREPENNLSLEDNRN 538
 DB 498 MCNSDNSSTAMLTDCIQOHAELNGMIPTDTKREPENNLSLEDNRN 543

RESULT 7
 ABB83542
 ID ABB83542 standard; protein; 543 AA.
 AC ABB83542;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Hypothalamus-expressed potassium channel protein.
 XX
 KW Hypothalamus; potassium channel; obesity; human.
 XX
 OS Homo sapiens.
 OS
 XX
 PN WO200252000-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 25-DEC-2001; 2001WO-JP011330.
 XX
 PR 26-DEC-2000; 2000JP-00396020.
 XX
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 PA
 XX
 PI Yokoi H, Inamura K, Sano Y, Miyake A, Mochizuki S;
 XX
 DR WPI, 2002-508889/54.
 DR N-PSDB; ABB85879.
 XX
 PT Hypothalamus-expressed potassium channel protein and encoded
 PT polynucleotide, applicable in screening inhibitors as anti-obestic agents
 PT to control food intake and enhanced energy consumption.
 XX
 PS Claim 1; Page 39-41; 45pp; Japanese.
 XX
 CC This invention relates to a hypothalamus-expressed protein having
 CC potassium channel activity. The protein and polynucleotide are applicable
 CC in screening inhibitors as anti-obesity agents to control food intake and
 CC enhanced energy consumption. The said screening process is advantageous
 CC as it is convenient to operate. This sequence represents a potassium
 CC channel activity protein
 XX
 SQ Sequence 543 AA;

Query Match 97.7%; Score 2697; DB 5; Length 543;
 Best Local Similarity 100.0%; Pred. No. 1.1e-238; Indels 0; Gaps 0;
 Matches 526; Conservative 0; Mismatches 0;

QY 13 VAVPAAAPVCPKSNATNGOPAPAPPTPTPLRSSRATVVARMEGTSQGLQTVNMKKTIV 72
 DB 18 VAVPAAAPVCPKSNATNGOPAPAPPTPTPLRSSRATVVARMEGTSQGLQTVNMKKTIV 77
 QY 73 VAIFVVVVVYLTGGLVFRALRQPESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132
 DB 78 VAIFVVVVVYLTGGLVFRALRQPESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137
 QY 133 DADNAGVSPIGNSNNSHWDIGSAFFPAGTIVTTIGYGNIAPISTEGGKIFCILYAFGI 192
 DB 138 DADNAGVSPIGNSNNSHWDIGSAFFPAGTIVTTIGYGNIAPISTEGGKIFCILYAFGI 197

RESULT 8

ADA05746

ID ADA05746 standard; protein; 543 AA.

AC ADA05746;

XX

DT 06-NOV-2003 (first entry)

XX

DE Human NOV19a protein SEQ ID NO:106.

XX

KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

XX

PN WO2003029424-A2.

XX

PD 10-APR-2003.

XX

PF 02-OCT-2002; 2002WO-US031373.

XX

PR 02-OCT-2001; 2001US-0326483P.

PR

PR 05-OCT-2001; 2001US-0327435P.

PR

PR 05-OCT-2001; 2001US-0327449P.

PR

PR 09-OCT-2001; 2001US-0327917P.

PR

PR 09-OCT-2001; 2001US-0328029P.

PR

PR 09-OCT-2001; 2001US-0328044P.

PR

PR 09-OCT-2001; 2001US-0328056P.

PR

PR 12-OCT-2001; 2001US-0328849P.

PR

PR 15-OCT-2001; 2001US-0329414P.

PR

PR 17-OCT-2001; 2001US-0330142P.

PR

PR 18-OCT-2001; 2001US-0330309P.

PR

PR 22-OCT-2001; 2001US-0341058P.

PR

PR 24-OCT-2001; 2001US-0339266P.

PR

PR 29-OCT-2001; 2001US-0349575P.

PR

PR 01-NOV-2001; 2001US-0346357P.

PR

PR 17-APR-2002; 2002US-0373260P.

PR

PR 19-APR-2002; 2002US-0373815P.

PR

PR 19-APR-2002; 2002US-0373817P.

PR

PR 19-APR-2002; 2002US-0373826P.

PR

PR 19-APR-2002; 2002US-0373884P.

PR

PR 22-APR-2002; 2002US-0374977P.

PR

PR 16-MAY-2002; 2002US-0381037P.

PR

PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patirajan M, Spytek KA, Edinger SR, Ellerman K, Malyanar UM;
 PI Ort T, Gorman L, Zernhusen BD, Anderson DW, Zhong M, Catterton B;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI: 2003-381626/36.
 DR N-PSDB; ADA05745.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 PT
 XX Claim 1; Page 176; 586pp; English.
 PS
 CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
 CC and antilipase activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 543 AA;
 Query Match 97.7%; Score 2697; DB 6; Length 543;
 Best Local Similarity 100.0%; Pred. No. 1.1e-238;
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 13 VAVFAAPVCPKATNGQPPAPAPTPTPLRISIRATVVARMEGTSGGLQTVWKTKV 72
 18 VAVFAAPVCPKATNGQPPAPAPTPTPLRISIRATVVARMEGTSGGLQTVWKTKV 77
 73 VAIFVVVVVLTGGLVFRALPEQPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHAL 132

DB 78 VAIFVVVVVLTGGLVFRALPEQPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHAL 137
 QY 133 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTAVTTTIGYGNIAPISTEGGKIFCILYAIFGI 192
 DB 138 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTAVTTTIGYGNIAPISTEGGKIFCILYAIFGI 197
 QY 193 PLFGFLLAGIGDQLCITFKGSIARVEKVPKQVQTKIRVISTITLIFILAGCIVFTTIPA 252
 DB 198 PLFGFLLAGIGDQLCITFKGSIARVEKVPKQVQTKIRVISTITLIFILAGCIVFTTIPA 257
 QY 253 VIFKIEGTALLESYFVWVLTITTVGDFVAGNAGINRYRWYKPLVWFWLVLGLAYFA 312
 DB 258 VIFKIEGTALLESYFVWVLTITTVGDFVAGNAGINRYRWYKPLVWFWLVLGLAYFA 317
 QY 313 AVLSMIGDMLRVLSKTKKEEVEIKAAHAAEWKANTVAFRETRRLRSVEIHDKQRAATI 372
 DB 318 AVLSMIGDMLRVLSKTKKEEVEIKAAHAAEWKANTVAFRETRRLRSVEIHDKQRAATI 377
 QY 373 RSMERRRLGLDQRAHSLDMLSPKESVFAALDTGPKASSQESINNRPNRLKGPQOLN 432
 DB 378 RSMERRRLGLDQRAHSLDMLSPKESVFAALDTGPKASSQESINNRPNRLKGPQOLN 437
 QY 433 KHGQGASEDNIIKFGSTSRITKRNKDLKKTLPEDVQIKYKTFRNYSLDESKRETEK 492
 DB 438 KHGQGASEDNIIKFGSTSRITKRNKDLKKTLPEDVQIKYKTFRNYSLDESKRETEK 497
 QY 493 MCNSDNSSTAMLTDCIQHAELENGMIPTDKOREPENNLSLEDNRN 538
 DB 498 MCNSDNSSTAMLTDCIQHAELENGMIPTDKOREPENNLSLEDNRN 543
 RESULT 9
 ADE08315
 ID ADE08315 standard; protein; 543 AA.
 AC ADE08315;
 XX
 XX 29-JAN-2004 (first entry)
 XX Novel protein (useful for identifying genetic disorders) #470.
 DE novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.
 XX
 OS Unidentified.
 XX
 PN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 DR WPI: 2003-569235/53.
 DR N-PSDB; ADE07404.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

XX Claim 20; SEQ ID NO 1381; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.

XX Sequence 543 AA;

Query Match 97.7%; Score 2697; DB 7; Length 543;
Best Local Similarity 100.0%; Pred. No. 1.1e-238; Mismatches 0; Gaps 0;
Matches 526; Conservative 0; Indels 0;

QY 13 VAVPAAAPVCPKSAATNGPPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKTIV 72
Db 18 VAVPAAAPVCPKSAATNGPPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKTIV 77
QY 73 VAIFVVVVVYLVGTGLVFRALQEPFESSQKNTTALKAFLRDHVCVSPQELTLIQHAL 132
Db 78 VAIFVVVVVYLVGTGLVFRALQEPFESSQKNTTALKAFLRDHVCVSPQELTLIQHAL 137
QY 133 DADNAGVSPIGNSSNNSSHWDLGSAPFFAGTIVTTTIGYGNIAPESTGGKIFCLYALFGI 192
Db 138 DADNAGVSPIGNSSNNSSHWDLGSAPFFAGTIVTTTIGYGNIAPESTGGKIFCLYALFGI 197
QY 193 PLFGFLLAGIDGDLGIFGKSIARVEKFRKQVSTQKIRVISTILFILAGCIVFVTIPA 252
Db 198 PLFGFLLAGIDGDLGIFGKSIARVEKFRKQVSTQKIRVISTILFILAGCIVFVTIPA 257
QY 253 VIFKYIEGTWALSIYFVVVVTLLTVGFGDFVAGNAGINREWKPLVFWILVGLAYFA 312
Db 258 VIFKYIEGTWALSIYFVVVVTLLTVGFGDFVAGNAGINREWKPLVFWILVGLAYFA 317
QY 313 AVLSMIGDMLRVLSKTKREVGSIKAAAEWKAHVTAEPRETRRLSVETHDKQRAAAT 372
Db 318 AVLSMIGDMLRVLSKTKREVGSIKAAAEWKAHVTAEPRETRRLSVETHDKQRAAAT 377
QY 373 RSMERRRLGIDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGPQLN 432
Db 378 RSMERRRLGIDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGPQLN 437
QY 433 KHGQGA SEDNI INKFGSTGRLTTRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKEBETEK 492
Db 438 KHGQGA SEDNI INKFGSTGRLTTRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKEBETEK 497
QY 493 MCNSDNSSTAMLTDCIQQAELNGLMPTDTKDREPENNSLLEDRN 538
Db 498 MCNSDNSSTAMLTDCIQQAELNGLMPTDTKDREPENNSLLEDRN 543

RESULT 10

ADN62910

ID ADN62910 standard; protein; 543 AA.

XX AC ADN62910;

XX DT 01-JUL-2004 (first entry)

XX DE Human NOV19a.

XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;

XX anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;

XX Alzheimer's disease; Parkinson's disease; immune disorder;

XX haematopoietic disorder; dyslipidaemia; metabolic syndrome X;

XX wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.
XX XX 26-FEB-2004.
XX PD
XX
XX 01-OCT-2002; 2002US-00262511.
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 05-OCT-2001; 2001US-0327449P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0339266P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374977P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381042P.
XX 28-MAY-2002; 2002US-0383656P.
XX 29-MAY-2002; 2002US-0383831P.
XX 25-JUN-2002; 2002US-0391335P.

XX (SMIT/) SMITHSON G.

PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.

PA (KEKU/) KEKUDA R.

PA (JUJU/) JU J.

PA (LILL/) LI L.

PA (GUOX/) GUO X.

PA (PATT/) PATTURAJAN M.

PA (SPYT/) SPYTEK K A.

PA (EDIN/) EDINGER S R.

PA (ELLE/) ELLERMAN K.

PA (MALY/) MALYANKAR U M.

PA (ORTT/) ORT T.

PA (GORM/) GORMAN L.

PA (ZERH/) ZERHUSEN B D.

PA (ANDE/) ANDERSON D W.

PA (ZHON/) ZHONG M.

PA (CATT/) CATTERTON E.

PA (JIWW/) JI W.

PA (MILL/) MILLER C E.

PA (RAST/) RASTELLI L.

PA (STON/) STONE D J.

PA (PENA/) PENA C B A.

PA (SHEN/) SHENOY S G.

PA (SHIM/) SHIMKETS R A.

PA (ROTH/) ROTHENBERG M E.

PA (LEAC/) LEACH M D.

PA (AGEE/) AGE E M L.

PA (BERG/) BERGHS C.

PA (DIPI/) DIPIPO V A.

PA (EISE/) EISEN A.

PA (GANG/) GANGOLLI E A.

PA (RIEG/) RIEGER D K.

PA (SPAD/) SPADERNA S K.

XX XX

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

PI Patturajan M, Spytek KA, Bainger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zethusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shency SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Elsen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX WPI; 2004-213931/20.
 DR N-PSDB; ADN62909.
 XX
 XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX
 PS Claim 1; SEQ ID NO.106; 395pp; English.
 XX

CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 543 AA;

Query Match 97.7%; Score 2697; DB 8; Length 543;
 Best Local Similarity 100.0%; Pred. No. 1.1e-238;
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 VAVPAAAPVCQPKSATNGQPPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKTIV 72
 Db 18 VAVPAAAPVCQPKSATNGQPPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKTIV 77
 QY 73 VAIFVWVYVLTGVLVFPALQPFSSQKNVIALEKAEFLRDHVCVSPQELTILQHAL 132
 Db 78 VAIFVWVYVLTGVLVFPALQPFSSQKNVIALEKAEFLRDHVCVSPQELTILQHAL 137
 QY 133 DADNAGVSPIGNSSNNSWDLGSAPFFAGTITVITIGYGNIAAPSTEGGKIFCILVAIRGI 192
 Db 138 DADNAGVSPIGNSSNNSWDLGSAPFFAGTITVITIGYGNIAAPSTEGGKIFCILVAIRGI 197
 QY 193 PLFGLLAGIGDQLGTIFGKSIAARVEKVFRRKQVSTKIRLVISTILFILAGCIVFVTIPA 252
 Db 198 PLFGLLAGIGDQLGTIFGKSIAARVEKVFRRKQVSTKIRLVISTILFILAGCIVFVTIPA 257
 QY 253 VIFKIEGHTALESIFVVTITVVGFGDFVAGNAGINRYRWYKPLVWFWILVGLAYPA 312
 Db 258 VIFKIEGHTALESIFVVTITVVGFGDFVAGNAGINRYRWYKPLVWFWILVGLAYPA 317
 QY 313 AVLSMIGDLRLVLSKTKKEVGEIKAAHAEWKNVTAETRETRRLSVIEHDKLQRAATI 372
 Db 318 AVLSMIGDLRLVLSKTKKEVGEIKAAHAEWKNVTAETRETRRLSVIEHDKLQRAATI 377

QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQBSQESINNRPNRLKRGPEQLN 432
 Db 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQBSQESINNRPNRLKRGPEQLN 437
 QY 433 KHGQGASEDNIINKFGSTSRLLTKRKQKOLKKTLPEDVQKIYKTFRNYSLDEEKKEBETEK 492
 Db 438 KHGQGASEDNIINKFGSTSRLLTKRKQKOLKKTLPEDVQKIYKTFRNYSLDEEKKEBETEK 497
 QY 493 MCNSDNSSTAMLTDCICQHAELNGMIPDTDKORPENNSLLEDRN 538
 Db 498 MCNSDNSSTAMLTDCICQHAELNGMIPDTDKORPENNSLLEDRN 543

RESULT 11

AAU79473

ID AAU79473 standard; protein; 543 AA.

AC AAU79473;

DT 15-JUL-2002 (first entry)

DE Human novel transporter protein variant.

KW Human; transporter; transgenic; transporter mediated disease;
 XX drug screening; pharmacogenomic analysis; chromosome 18.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 233

PT /note= "Wild-type Gln substituted by Lys"

XX WO200224748-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US029211.

XX 19-SEP-2000; 2000US-0233663P.

XX 06-DEC-2000; 2000US-00729920.

XX (PEXE) PE CORP NY.

XX Guegler K, Ketchum KA, Di Francesco V, Beasley EM;

XX WPI; 2002-351999/38.

XX New human transporter proteins and nucleic acids, useful as models in the
 PT development of human therapeutic agents, in identifying therapeutic
 PT proteins, or as query sequence in database searches to identify related
 PT sequences.

XX Disclosure; Page; 207pp; English.

XX The invention relates to a new isolated peptide being a human transporter
 CC protein, an allelic variant, orthologue, fragment or sequence that is 70%
 CC homologous to the transporter. Also included are a nucleic acid encoding
 CC the transporter (including allelic variants, orthologue, fragment or
 CC complement), an antibody against the protein, a gene chip comprising the
 CC nucleic acids, a transgenic non-human animal comprising the nucleic
 CC acids, a nucleic acid vector comprising the nucleic acids, a host cell
 CC containing the vector, identifying agents that bind to and/or modulate
 CC the function of the transporter, and treating a disease or condition
 CC mediated by a human transporter protein by administering to the patient
 CC an identified agent or modulator. The peptide sequences and the nucleic
 CC acid sequences encoding these peptides can be used as models for the
 CC development of human therapeutic targets, aid in the identification of
 CC therapeutic proteins, and serve as targets for the development of human
 CC therapeutic agents that modulate transporter activity in cells and
 CC tissues that express the transporter. These sequences may also be used as
 CC query sequence in database searches to identify other family members or
 CC related sequences. The proteins may be used to raise antibodies or to
 CC elicit immune response, as a reagent in assays designed to quantitatively

CC determine protein levels in biological fluids; as markers for tissues in
 CC which the corresponding protein is expressed; in drug screening assays in
 CC cell-based or cell-free systems; to identify compounds that modulate
 CC transporter activity of the protein in its natural state or altered form
 CC that causes a specific disease or pathology associated with the
 CC transporter; as target for diagnosing a disease or predisposition to
 CC disease mediated by the peptide; and in pharmacogenomic analysis. The
 CC nucleic acids are useful as hybridisation probes or primers; in
 CC monitoring the effectiveness of modulating compounds on the expression or
 CC activity of the transporter gene in clinical trials or treatment regimen;
 CC in diagnostic assays for qualitative changes in transporter nucleic acid
 CC expression; and as antisense constructs. The gene for the transporter is
 CC located on chromosome 18. The present sequence represents a variant of
 CC the novel human transporter. Note: The present sequence is not shown in
 CC the specification but was created by the indexer from the information in
 CC figure 3 and the transporter sequence appearing as AAU79472

XX SQ Sequence 543 AA;

Query Match 97.6%; Score 2693; DB 5; Length 543;
 Best Local Similarity 99.8%; Pred. No. 2.5e-238;
 Matches 525; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCQPKSATNGQPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKT 72
 DB 18 VAVPAAAPVCQPKSATNGQPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKT 77
 QY 73 VAIFVVVVVYLVGTGLVFRALPEPSSQKNTIALEKAEFLRDHVCVSPQELTLOHAL 132
 DB 78 VAIFVVVVVYLVGTGLVFRALPEPSSQKNTIALEKAEFLRDHVCVSPQELTLOHAL 137
 QY 133 DADNAGVSPIGNSSNNSHWDLGSAFFAGTGTITTYGNIAPSTEGGKIFCLLYAIFGI 192
 DB 138 DADNAGVSPIGNSSNNSHWDLGSAFFAGTGTITTYGNIAPSTEGGKIFCLLYAIFGI 197
 QY 193 PLFGFLAGIGDQGLTIFGKSIARVEKVPKQVSGTQKIRVISTILFILAGCIVFVTIPA 252
 DB 198 PLFGFLAGIGDQGLTIFGKSIARVEKVPKQVSGTQKIRVISTILFILAGCIVFVTIPA 257
 QY 253 VIFKYEIGWTALESIFVYVVTITVTGFGDFVAGNAGINRYEYKPLVFWFVLGLAYFA 312
 DB 258 VIFKYEIGWTALESIFVYVVTITVTGFGDFVAGNAGINRYEYKPLVFWFVLGLAYFA 317
 QY 313 AVLSMIGDMLRVLSKTKKEVGEIKAAAEWKANVTAEFRTTTRRLSVETIHDKLOAAAT 372
 DB 318 AVLSMIGDMLRVLSKTKKEVGEIKAAAEWKANVTAEFRTTTRRLSVETIHDKLOAAAT 377
 QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGPQELN 432
 DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGPQELN 437
 QY 433 KHQCGASEDNIIKFGSTSLTRKNDLKKTIPEVQKIYKTFRNYSLDEEKKBEETEK 492
 DB 438 KHQCGASEDNIIKFGSTSLTRKNDLKKTIPEVQKIYKTFRNYSLDEEKKBEETEK 497
 QY 493 MCNSDMSSTAMLTDCIQOHAELNGMPTDTKDREPENNSLLSDRN 538
 DB 498 MCNSDMSSTAMLTDCIQOHAELNGMPTDTKDREPENNSLLSDRN 543

RESULT 12

AAO14193

ID AAO14193 standard; protein; 724 AA.

XX AC AAO14193;

XX AC AAO14193;

DT 03-MAY-2002 (first entry)

XX Human transporter and ion channel TRICH-10.

XX Human; transporter and ion channel; TRICH; transport disorder;

XX neurological disorder; muscle disorder; immunological disorder;

KW cell proliferative disorder; neuroprotective; nootropic;

KW cerebroprotective; immunosuppressive; cytostatic; respiratory; muscular;
 KW gene therapy.

XX Homo sapiens.

XX WO200204520-A2.

XX 17-JAN-2002.

XX 05-JUL-2001; 2001WO-US021448.

XX 07-JUL-2000; 2000US-0216547P.

XX 14-JUL-2000; 2000US-0218232P.

XX 21-JUL-2000; 2000US-0220112P.

XX 28-JUL-2000; 2000US-0221839P.

XX (INCY-) INCYTE GENOMICS INC.

XX Raumann BE, Thornton M, Ding L, Yue H, Tang YT, Harland L;

XX Burford N, Greene BD, Sanjanwala MS, Baughn MR, Yao MG, Yang J;

XX Patterson C, Gandhi AR, Hafalia AJA, Tribouley CM, Walia NK;

XX Au-Young J, Walsh RT, Ramkumar J, Lu Y, Lu DAM, Azimzai Y, Lal P;

XX Elliott VS, Nguyen DB, Xu Y, Seilhamer JJ, Borowsky ML, Khan FA;

XX Kearney L, Thangavelu K, Das D, Policky JL;

XX WPI; 2002-205969/26.

XX N-PSDB; AAL44676.

XX New human transporters and ion channel polypeptides for diagnosing,

XX treating or preventing transport, neurological, muscle, immunological and

XX cell proliferative disorders.

XX Claim 1; Page 158-160; 230pp; English.

XX The present invention provides the protein and coding sequences of a

XX number of human transporters and ion channel proteins, designated TRICH-1-

XX TRICH-32. The sequences can be used in the treatment of transport,

XX neurological, muscle, immunological and cell proliferative disorders. The

XX present sequence is a protein of the invention

XX Sequence 724 AA;

XX Query Match 96.3%; Score 2657.5; DB 5; Length 724;

XX Best Local Similarity 98.7%; Pred. No. 7e-235;

XX Matches 523; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

QY 13 VAVPAAAPVCQPKSATNGQPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKT 72

DB 196 VAVPAAAPVCQPKSATNGQPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKT 255

QY 73 VAIFVVVVVYLVGTGLVFRALPEPSSQKNTIALEKAEFLRDHVCVSPQELTLOHAL 132

DB 256 VAIFVVVVVYLVGTGLVFRALPEPSSQKNTIALEKAEFLRDHVCVSPQELTLOHAL 315

QY 133 DADNAGVSPIGNSSNNSHWDLGSAFFAGTGTITTYGNIAPSTEGGKIFCLLYAIFGI 192

DB 316 DADNAGVSPIGNSSNNSHWDLGSAFFAGTGTITTYGNIAPSTEGGKIFCLLYAIFGI 374

QY 193 PLFGFLAGIGDQGLTIFGKSIARVEKVPKQVSGTQKIRVISTILFILAGCIVFVTIPA 252

DB 375 PLFGFLAGIGDQGLTIFGKSIARVEKVPKQVSGTQKIRVISTILFILAGCIVFVTIPA 434

QY 253 VIFKYEIGWTALESIFVYVVTITVTGFGDFVAGNAGINRYEYKPLVFWFVLGL 308

DB 435 VIFKYEIGWTALESIFVYVVTITVTGFGDFVAGNAGINRYEYKPLVFWFVLGL 494

QY 309 AYFAAVLSMIGDMLRVLSKTKKEVGEIKAAAEWKANVTAEFRTTTRRLSVETIHDKLO 368

DB 495 AYFAAVLSMIGDMLRVLSKTKKEVGEIKAAAEWKANVTAEFRTTTRRLSVETIHDKLO 554

QY 369 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGP 428

DB 555 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGP 614

QY 429 EQLNKHGQASDNIINKFGSTSRLLTKRKNKOLKKTLPEDVQKIYKTFNYSLSDEKKEE 488
 |||||
 Db 615 EQLNKHGQASDNIINKFGSTSRLLTKRKNKOLKKTLPEDVQKIYKTFNYSLSDEKKEE 674
 |||||
 QY 489 ETEKMCNSDNTAMLTDCIQOHAELNGMIPDTTKREPENNSLLEDRN 538
 |||||
 Db 675 ETEKMCNSDNTAMLTDCIQOHAELNGMIPDTTKREPENNSLLEDRN 724
 |||||

RESULT 13

ABG02731
 ID ABG02731 standard; protein; 383 AA.

XX AC
 XX ABG02731;

DT DT
 XX 13-FEB-2002 (first entry)

DE DE
 XX Novel human diagnostic protein #2722.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX

OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS66918.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 33090; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG03077 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 383 AA;

Query Match 59.1%; Score 1630; DB 4; Length 383;

Best Local Similarity 100.0%; Pred. No. 8.8e-141;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 RKQVQSOTKIRVISTILFILACGIVFVTPAVIFKYIEGWTALSIYFVVTLTTVGFGD 281

Db 67 RKQVQSOTKIRVISTILFILACGIVFVTPAVIFKYIEGWTALSIYFVVTLTTVGFGD 126

QY 282 FVAGGNAGINREWKPLVFWFVLVGLAYFAAVALSMIGDMLVLSKTKKEEVEIGIKAHAA 341

Db 127 FVAGGNAGINREWKPLVFWFVLVGLAYFAAVALSMIGDMLVLSKTKKEEVEIGIKAHAA 186

QY 342 EWKANVTAEFRTRRLRSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKKSQVFA 401

Db 187 EWKANVTAEFRTRRLRSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKKSQVFA 246

QY 402 ALDTCRPFKASSQESINNRPNRLKGPOLNKHGQASDNIINKFGSTSRLLTKRKNKOL 461

Db 247 ALDTCRPFKASSQESINNRPNRLKGPOLNKHGQASDNIINKFGSTSRLLTKRKNKOL 306

QY 462 KKTLPEDVQKIYKTFNYSLSDEKKEEETKMCNSDNTAMLTDCIQOHAELNGMIP 521

Db 307 KKTLPEDVQKIYKTFNYSLSDEKKEEETKMCNSDNTAMLTDCIQOHAELNGMIP 366

QY 522 DTKREPENNSLLEDRN 538

Db 367 DTKREPENNSLLEDRN 383

RESULT 14

ABG08305

ID ABG08305 standard; protein; 557 AA.

XX AC ABG08305;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #8296.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX

OS Homo sapiens.

XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS72492.

XX New isolated polynucleotide and encoded polypeptides, useful in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits and to assess
 CC biodiversity.

XX Claim 20; SEQ ID NO 38664; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (ii) and its binding partners are useful in medical imaging
 CC of sites expressing (ii). (i) and (ii) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 557 AA;

Query Match 51.2%; Score 1412.5; DB 4; Length 557;
 Best Local Similarity 72.4%; Pred. No. 1.6e-120;
 Matches 297; Conservative 2; Mismatches 18; Indels 93; Gaps 4;
 QY 222 RKQVSGTKIRVISTILFILAGCIVFTIPAVIFKIEGWTALSYFVVVTLTTVGGFD 281
 DB 148 QKQVSGTKIRVISTILFILAGCIVFTIPAVIFKIEGWTALSYFVVVTLTTVGGFD 207
 QY 282 FVAG-----GNAGINIREWYKPLVWFIL----- 305
 DB 208 FVAHPSDHLCWIVTVCKGYLLPDSPOEKATDFSGVAKNEPQKPLINWELRSYPTA 267
 QY 306 -----VGLAYFA-AVLNMGIDWLRVLSKTK 330
 DB 268 LMQERVWVKKPKAAANRRRLGTEKLEFPXREVAAPVAVLHSMIGDWRVLSKTK 327
 QY 331 EE-----VGEIKAAHAEWKANTAEPRTRRLSVLEHDKLOR 368
 DB 328 EYVCRPLFKSPNRLRLGLVAHVHGEIKAAHAEWKANTAEPRTRRLSVLEHDKLOR 387
 QY 369 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRPKASSQBSINNRPNRLKGP 428
 DB 388 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRPKASSQBSINNRPNRLKGP 447
 QY 429 EQLNKHGQGAASENIINKFGSTSRRLTKRNKDLKTLPEVDQKIYKTFNYSLEDEKKEE 488
 DB 448 EQLNKHGQGAASENIINKFGSTSRRLTKRNKDLKTLPEVDQKIYKTFNYSLEDEKKEE 507
 QY 489 ETEKMCNDSNSTAMLTDCIQHAELENGMIPDTVDREPNNSLLEDRN 538
 DB 508 ETEKMCNDSNSTAMLTDCIQHAELENGMIPDTVDREPNNSLLEDRN 557

RESULT 15

AAE10342
 ID AAE10342 standard; protein; 411 AA.

XX
 AC AAE10342;

XX
 DT 10-DEC-2001 (first entry)

XX
 DE Murine TREK-1 potassium channel protein.

XX
 KW Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;
 KW amnesia.

XX
 OS Mus musculus.

XX
 PN WO200047738-A2.

XX
 PD 17-AUG-2000.

XX
 PF 11-FEB-2000; 2000WO-IB000226.

XX
 PR 12-FEB-1999; 99US-0119727P.

PR 11-FEB-2000; 2000US-00503089.

XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;
 XX
 XX WPI; 2000-549146/50.
 DR N-PSDB; AAD17497.
 XX
 XX Novel nucleic acid encoding a TREK-1 potassium channel protein for
 PT transfecting cells to be used to identify compounds with anesthetic
 PT properties.
 XX
 PS Claim 9; Page 32-33; 39pp; English.
 XX
 XX The invention relates to human and mouse TREK-1 potassium channel
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
 CC useful for transfecting cells to induce expression of the TREK-1
 CC potassium channel protein. These cells are then used in assays to
 CC identify compounds which have anesthetic properties, producing a safe,
 CC reversible state of unconsciousness with concurrent amnesia and analgesia
 CC in a mammal upon inhalation. The present sequence is murine TREK-1
 CC potassium channel protein
 XX
 SQ Sequence 411 AA;

Query Match 45.3%; Score 1251.5; DB 3; Length 411;
 Best Local Similarity 64.3%; Pred. No. 6.4e-106;
 Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;
 QY 17 AAAPVCQPKSANGPPAPAPPTPTRLSISRSATVVA-RMEGTSQGLQTVMKWKTVAI 75
 DB 2 AAPDLLDPKSA-----AQNSKPLSPSSKPTVLASRVESDS---AINVMKWKTVSTI 50
 QY 76 FVVVVVYLVTVGLVFRALQEPSESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDAD 135
 DB 51 FLVVVLYLILGAAVFAKALEQPOEISQRTTIVIQKOTFFIAQHACVNSTEDELIIQIIVAAI 110
 QY 136 NAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIIGYGNIAPTSTEGGKIFCIIYALGIPLF 195
 DB 111 NAGIPLGNSSNQVSHWDLGSSFFAGTVITTIIGYGNISPTTEGGKIFCIIYALGIPLF 170
 QY 196 GFLLAGIGDQLGTIFGKSIARVEKVFRRKQVSGTKIRVISTILFILAGCIVFTTIPAVIF 255
 DB 171 GFLLAGVGDQLGTIFGKGIKVEDTFIKWVNSQTKIRIISTIIIFILFGCVLFVALPAVIF 230
 QY 256 KYIEGWTALSYFVVVTLTTVGGDFVAGGNAGINIREWYKPLVWFILVGLAYFAAVL 315
 DB 231 KHIEGWSALDAILYFVVITLTTIGFDYVAGG-SDIEYLDYFKPVVWFWILVGLAYFAAVL 289
 QY 316 SMIGDWLRVLSKTKBEVGEIKAAHAEWKANTAEPRTRRLSVLEHDKLQRAAATIRSM 375
 DB 290 SMIGDWLRVLSKTKBEVGEIPEFAHAAEWNTANTAEPRTRRLSVLEHDKLQRAAATIRSM 346
 QY 376 EERRRLGLDQRAHSLDMLSPKRSV 399
 DB 347 -KKKLSAELAGNHNQELTPCRRTL 369

Search completed: April 28, 2005, 13:25:15
 Job time : 166 secs

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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:26:07 ; Search time 134 Seconds
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Title: US-09-892-360-2
Perfect score: 2760
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Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues
Total number of hits satisfying chosen parameters: 1426032

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		Description	
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1	2760	100.0	538	11	US-09-892-360-2	Sequence 2, Appli	
2	2697	97.7	526	9	US-09-729-920-4	Sequence 4, Appli	
3	2697	97.7	543	9	US-09-729-920-2	Sequence 2, Appli	
4	2697	97.7	543	10	US-09-852-386-73	Sequence 73, Appli	
5	2697	97.7	543	14	US-10-332-175-2	Sequence 2, Appli	
6	2697	97.7	543	15	US-10-262-511-106	Sequence 106, App	
7	2657.5	96.3	724	15	US-10-332-447-10	Sequence 10, Appli	
8	2560.5	92.8	538	9	US-09-729-920-5	Sequence 5, Appli	
9	1248.5	45.2	411	9	US-09-828-746-6	Sequence 6, Appli	
10	1243	45.0	411	11	US-09-892-360-18	Sequence 18, Appli	
11	1242.5	45.0	411	9	US-09-828-746-2	Sequence 2, Appli	
12	1242.5	45.0	411	14	US-10-121-746-83	Sequence 83, Appli	
13	1242.5	45.0	411	16	US-10-745-210-2	Sequence 2, Appli	

14	1238.5	44.9	370	9	US-09-939-484-8	Sequence 8, Appli	
15	1238.5	44.9	370	9	US-09-939-483-8	Sequence 8, Appli	
16	1218.5	44.1	426	8	US-08-816-011-45	Sequence 45, Appli	
17	1218.5	44.1	426	17	US-10-870-492-45	Sequence 57, Appli	
18	1218.5	44.1	426	17	US-10-870-492-57	Sequence 58, Appli	
19	1214.5	44.0	426	17	US-10-870-492-58	Sequence 59, Appli	
20	1210.5	43.9	426	17	US-10-870-492-59	Sequence 60, Appli	
21	1210.5	43.9	426	17	US-10-870-492-60	Sequence 29, Appli	
22	825.5	29.9	1314	9	US-09-747-835A-29	Sequence 2, Appli	
23	825.5	29.9	1314	15	US-10-312-312-29	Sequence 44, Appli	
24	822.5	29.8	419	9	US-09-828-035-2	Sequence 29, Appli	
25	822.5	29.8	419	14	US-10-345-680-44	Sequence 8, Appli	
26	822.5	29.8	419	14	US-10-146-733-29	Sequence 19, Appli	
27	822.5	29.8	419	15	US-10-352-684A-8	Sequence 55, Appli	
28	822.5	29.8	419	15	US-10-331-399-19	Sequence 19, Appli	
29	812.5	29.4	392	9	US-09-747-835A-55	Sequence 2599, App	
30	812.5	29.4	392	15	US-10-312-312-55	Sequence 2, Appli	
31	812.5	29.4	393	14	US-10-243-035-2	Sequence 2, Appli	
32	790	28.6	398	11	US-09-892-360-19	Sequence 172, App	
33	610.5	22.1	421	15	US-10-276-774-2599	Sequence 177, App	
34	512	18.6	294	13	US-10-121-566-2	Sequence 11, Appli	
35	512	18.6	294	15	US-10-451-892-2	Sequence 10, Appli	
36	512	18.6	294	15	US-10-459-190-2	Sequence 4, Appli	
37	512	18.6	294	15	US-10-459-190-9	Sequence 2, Appli	
38	512	18.6	309	15	US-10-080-334-172	Sequence 17, App	
39	512	18.6	309	15	US-10-080-334-177	Sequence 177, App	
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43	511	18.5	292	15	US-10-459-190-4	Sequence 2, Appli	
44	483	17.5	499	9	US-09-735-169A-2	Sequence 2, Appli	
45	483	17.5	499	9	US-09-735-171A-2	Sequence 2, Appli	

ALIGNMENTS

RESULT 1
US-09-892-360-2
; Sequence 2, Application US/09892360
; Publication No. US20040101833A1
; GENERAL INFORMATION:
; APPLICANT: LAZUNSKI, MICHAEL
; APPLICANT: LESUNGE, FLORENCE
; APPLICANT: ROMEY, GEORGES
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
; TITLE OF INVENTION: RILUZOLE
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-360-2

Query Match 100.0%; Score 2760; DB 11; Length 538;
Best Local Similarity 100.0%; Pred. No. 3.7e-216;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFLLYDFFLSLVAVPAAPVCPKSNATNGOPPAPATPTPTPLSISSRATVVARMEGTSQ 60
Db 1 MFLLYDFFLSLVAVPAAPVCPKSNATNGOPPAPATPTPTPLSISSRATVVARMEGTSQ 60
Qy 61 GGLQTMKMTVAIFVWVYLVVTGLVFRALPEQPPESSQKNTIALEKAEFLRDHVCVS 120
Db 61 GGLQTMKMTVAIFVWVYLVVTGLVFRALPEQPPESSQKNTIALEKAEFLRDHVCVS 120

QY 121 POELETLIQHALDADNAGVSPICGNSNNSSHWDLGSAFFAGTAVTTTIGYGNIAFSTEGG 180
 DB 121 POELETLIQHALDADNAGVSPICGNSNNSSHWDLGSAFFAGTAVTTTIGYGNIAFSTEGG 180
 QY 181 KIFCILYAIIFGFLPGLAGIDGOLGTFGKSIARVEKVFPRKQVSTKIRVISTILFI 240
 DB 181 KIFCILYAIIFGFLPGLAGIDGOLGTFGKSIARVEKVFPRKQVSTKIRVISTILFI 240
 QY 241 LAGCIVFVTIPAVIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLV 300
 DB 241 LAGCIVFVTIPAVIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLV 300
 QY 301 WFWILVGLAYFAAVALSMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSV 360
 DB 301 WFWILVGLAYFAAVALSMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSV 360
 QY 361 EIHDKLORAAATIRSMERRRGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
 DB 361 EIHDKLORAAATIRSMERRRGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
 QY 421 NNLRKGPOLNKGQASGSEDIINFKGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 480
 DB 421 NNLRKGPOLNKGQASGSEDIINFKGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 480
 QY 481 LDEEKKKEETERKMCNSDSTAMLTDCIQOHAELNGMIPTDTKOREPENNSLLEDN 538
 DB 481 LDEEKKKEETERKMCNSDSTAMLTDCIQOHAELNGMIPTDTKOREPENNSLLEDN 538

RESULT 2

US-09-729-920-4
 ; Sequence 4, Application US/09729920
 ; Patent No. US20020103115A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
 ; FILE REFERENCE: CL000858
 ; CURRENT APPLICATION NUMBER: US/09/729,920
 ; CURRENT FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 526
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-729-920-4

Query Match 97.7%; Score 2697; DB 9; Length 526;
 Best Local Similarity 100.0%; Pred. No. 4.9e-211;
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATNGPPAPAPPTPRLSISSRATVVARMEGTSGGLQTVMKWKT 72
 DB 1 VAVPAAAPVCPKSAATNGPPAPAPPTPRLSISSRATVVARMEGTSGGLQTVMKWKT 60
 QY 73 VAIFVWVWVYLVGTGLVFRALQPPSSQKNTIALEKAEFLRDHVCVSPQLETLIOHAL 132
 DB 61 VAIFVWVWVYLVGTGLVFRALQPPSSQKNTIALEKAEFLRDHVCVSPQLETLIOHAL 120
 QY 133 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTAVTTTIGYGNIAFSTEGGKIFCILYAI 192
 DB 121 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTAVTTTIGYGNIAFSTEGGKIFCILYAI 180
 QY 193 PLFGFLLAGIDGOLGTFGKSIARVEKVFPRKQVSTKIRVISTILFILAGCIVFTIPA 252
 DB 181 PLFGFLLAGIDGOLGTFGKSIARVEKVFPRKQVSTKIRVISTILFILAGCIVFTIPA 240
 QY 253 VIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLVFWFVILVGLAYFA 312
 DB 241 VIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLVFWFVILVGLAYFA 300

QY 313 AVLWMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSVIEIHDKLQRAATI 372
 DB 301 AVLWMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSVIEIHDKLQRAATI 360
 QY 373 RSMERRRGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPQLN 432
 DB 361 RSMERRRGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPQLN 420
 QY 433 KHGQASGSEDIINFKGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKKEET 492
 DB 421 KHGQASGSEDIINFKGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKKEET 480
 QY 493 MCNSDSTAMLTDCIQOHAELNGMIPTDTKOREPENNSLLEDN 538
 DB 481 MCNSDSTAMLTDCIQOHAELNGMIPTDTKOREPENNSLLEDN 526

RESULT 3

US-09-729-920-2
 ; Sequence 2, Application US/09729920
 ; Patent No. US20020103115A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
 ; FILE REFERENCE: CL000858
 ; CURRENT APPLICATION NUMBER: US/09/729,920
 ; CURRENT FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 543
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-729-920-2

Query Match 97.7%; Score 2697; DB 9; Length 543;
 Best Local Similarity 100.0%; Pred. No. 5.1e-211;
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATNGPPAPAPPTPRLSISSRATVVARMEGTSGGLQTVMKWKT 72
 DB 18 VAVPAAAPVCPKSAATNGPPAPAPPTPRLSISSRATVVARMEGTSGGLQTVMKWKT 77
 QY 73 VAIFVWVWVYLVGTGLVFRALQPPSSQKNTIALEKAEFLRDHVCVSPQLETLIOHAL 132
 DB 78 VAIFVWVWVYLVGTGLVFRALQPPSSQKNTIALEKAEFLRDHVCVSPQLETLIOHAL 137
 QY 133 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTAVTTTIGYGNIAFSTEGGKIFCILYAI 192
 DB 138 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTAVTTTIGYGNIAFSTEGGKIFCILYAI 197
 QY 193 PLFGFLLAGIDGOLGTFGKSIARVEKVFPRKQVSTKIRVISTILFILAGCIVFTIPA 252
 DB 198 PLFGFLLAGIDGOLGTFGKSIARVEKVFPRKQVSTKIRVISTILFILAGCIVFTIPA 257
 QY 253 VIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLVFWFVILVGLAYFA 312
 DB 258 VIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLVFWFVILVGLAYFA 317
 QY 313 AVLWMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSVIEIHDKLQRAATI 372
 DB 318 AVLWMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSVIEIHDKLQRAATI 377
 QY 373 RSMERRRGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPQLN 432
 DB 378 RSMERRRGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPQLN 437
 QY 433 KHGQASGSEDIINFKGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKKEET 492
 DB 438 KHGQASGSEDIINFKGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKKEET 497

QY 493 MCNSDSSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 538
DB 498 MCNSDSSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 543

RESULT 4

US-09-852-386-73
; Sequence 73, Application US/09852386
; Publication No. US2003064433A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Steven L.
; APPLICANT: Benjamin, Christopher
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Rubie, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00133.US1
; CURRENT APPLICATION NUMBER: US/09/852,386
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,305
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/207,092
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/206,526
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,033
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,093
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/216,893
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/207,873
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 60/223,245
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 73
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-386-73

Query Match 97.7%; Score 2697; DB 10; Length 543;
Best Local Similarity 100.0%; Pred. No. 5.1e-211;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSNATNGQPPAPAPPTPTPLRISISSRATVVARMEGTSGGLQTVMKWKT 72
DB 18 VAVPAAAPVCPKSNATNGQPPAPAPPTPTPLRISISSRATVVARMEGTSGGLQTVMKWKT 77

QY 73 VAVFVVVVVYLVGTGLVFRALRQPPESOKNTIALEKAEFLRDHVCVSPQLETLIOHAL 132
DB 78 VAVFVVVVVYLVGTGLVFRALRQPPESOKNTIALEKAEFLRDHVCVSPQLETLIOHAL 137

QY 133 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTVITIGYGNIAPTSTEGGKIFCILYAI FGI 192
DB 138 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTVITIGYGNIAPTSTEGGKIFCILYAI FGI 197

QY 193 PLFGFLLAGIDQLGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPA 252
DB 198 PLFGFLLAGIDQLGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPA 257

QY 253 VIFKYIEGWTALESYIFVWVTLTTVGFDFVAGGNAGINREWKPLWFWILVGLAYFA 312
DB 258 VIFKYIEGWTALESYIFVWVTLTTVGFDFVAGGNAGINREWKPLWFWILVGLAYFA 317

QY 313 AVLSMIGDMLRVLSKTKKEEVEGEIKAAHAEKANKVTAETFRTRRLSVEIHDKQRAATI 372
DB 318 AVLSMIGDMLRVLSKTKKEEVEGEIKAAHAEKANKVTAETFRTRRLSVEIHDKQRAATI 377

QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNRLKGPQOLN 432
DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNRLKGPQOLN 437

QY 493 MCNSDSSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 538
DB 498 MCNSDSSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 543

RESULT 6

US-10-262-511-106
; Sequence 106, Application US/10262511

QY 433 KHGOGASEDNIIKFGSTSRLLTKRKNKDLKTKLPEDVQKIYKTFRNYSLDEKKESETEK 492
DB 438 KHGOGASEDNIIKFGSTSRLLTKRKNKDLKTKLPEDVQKIYKTFRNYSLDEKKESETEK 497

QY 493 MCNSDSSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 538
DB 498 MCNSDSSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 543

RESULT 5

US-10-332-175-2
; Sequence 2, Application US/10332175
; Publication No. US20030176342A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. US20030176342A1el potassium channel
; FILE REFERENCE: Y013PCT-666
; CURRENT APPLICATION NUMBER: US/10/332,175
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: JP 2000-396020
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-332-175-2

Query Match 97.7%; Score 2697; DB 14; Length 543;
Best Local Similarity 100.0%; Pred. No. 5.1e-211;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSNATNGQPPAPAPPTPTPLRISISSRATVVARMEGTSGGLQTVMKWKT 72
DB 18 VAVPAAAPVCPKSNATNGQPPAPAPPTPTPLRISISSRATVVARMEGTSGGLQTVMKWKT 77

QY 73 VAVFVVVVVYLVGTGLVFRALRQPPESOKNTIALEKAEFLRDHVCVSPQLETLIOHAL 132
DB 78 VAVFVVVVVYLVGTGLVFRALRQPPESOKNTIALEKAEFLRDHVCVSPQLETLIOHAL 137

QY 133 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTVITIGYGNIAPTSTEGGKIFCILYAI FGI 192
DB 138 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTVITIGYGNIAPTSTEGGKIFCILYAI FGI 197

QY 193 PLFGFLLAGIDQLGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPA 252
DB 198 PLFGFLLAGIDQLGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPA 257

QY 253 VIFKYIEGWTALESYIFVWVTLTTVGFDFVAGGNAGINREWKPLWFWILVGLAYFA 312
DB 258 VIFKYIEGWTALESYIFVWVTLTTVGFDFVAGGNAGINREWKPLWFWILVGLAYFA 317

QY 313 AVLSMIGDMLRVLSKTKKEEVEGEIKAAHAEKANKVTAETFRTRRLSVEIHDKQRAATI 372
DB 318 AVLSMIGDMLRVLSKTKKEEVEGEIKAAHAEKANKVTAETFRTRRLSVEIHDKQRAATI 377

QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNRLKGPQOLN 432
DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNRLKGPQOLN 437

QY 433 KHGOGASEDNIIKFGSTSRLLTKRKNKDLKTKLPEDVQKIYKTFRNYSLDEKKESETEK 492
DB 438 KHGOGASEDNIIKFGSTSRLLTKRKNKDLKTKLPEDVQKIYKTFRNYSLDEKKESETEK 497

QY 493 MCNSDSSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 538
DB 498 MCNSDSSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 543


```
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spyttek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIORITY APPLICATION NUMBER: 60/326,483
PRIORITY FILING DATE: 2001-10-02
PRIORITY APPLICATION NUMBER: 60/373,815
PRIORITY FILING DATE: 2002-04-19
PRIORITY APPLICATION NUMBER: 60/327,917
PRIORITY FILING DATE: 2001-10-09
PRIORITY APPLICATION NUMBER: 60/381,642
PRIORITY FILING DATE: 2002-05-17
PRIORITY APPLICATION NUMBER: 60/328,029
PRIORITY FILING DATE: 2002-10-09
PRIORITY APPLICATION NUMBER: 60/381,038
PRIORITY FILING DATE: 2002-05-16
PRIORITY APPLICATION NUMBER: 60/328,056
PRIORITY FILING DATE: 2001-10-09
PRIORITY APPLICATION NUMBER: 60/373,260
PRIORITY FILING DATE: 2002-04-17
PRIORITY APPLICATION NUMBER: 60/373,826
PRIORITY FILING DATE: 2002-04-19
PRIORITY APPLICATION NUMBER: 60/327,435
PRIORITY FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 106
LENGTH: 543
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-106

Query Match 97.7%; Score 2697; DB 15; Length 543;
Best Local Similarity 100.0%; Pred. No. 5.1e-211;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATGPPAPPTPTPLSTSSRATVVARMGTSQGLQTVMKWKTIV 72
DB 18 VAVPAAAPVCPKSAATGPPAPPTPTPLSTSSRATVVARMGTSQGLQTVMKWKTIV 77
QY 73 VAIFVVVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHAL 132

Publication No. US20040053258A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; RAUMANN, Brigitte E.;
APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
APPLICANT: TANG, Y. Tom; HARLAND, Lee; BURFORD, Neil;
APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;
APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;
APPLICANT: HAFALIA, April J.A.; TRIBOULEY, Catherine M.;
APPLICANT: WALSH, Roderick T.; RAMKUMAR, Javalaxmi;
APPLICANT: LU, Yan; LU, Dyung Aina M.; AZIMZAI, Yalda;
APPLICANT: LAL, Preeti; ELLIOTT, Vicki S.; NGUYEN, Dannel B.;
APPLICANT: XU, Yuming; SEILHAMER, Jeffrey J.; BOROWSKY, Mark L.;
APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANGAVELU, Kavitha;
APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: PI-0149 USN
CURRENT APPLICATION NUMBER: US/10/332,447
CURRENT FILING DATE: 2003-01-07
PRIORITY APPLICATION NUMBER: US 60/216,547
PRIORITY FILING DATE: 2000-07-07
PRIORITY APPLICATION NUMBER: US 60/218,232
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 60/220,112
PRIORITY FILING DATE: 2000-07-21
PRIORITY APPLICATION NUMBER: US 60/221,839
PRIORITY FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 724
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040053258A1 7472728CDI
US-10-332-447-10

RESULT 7
US-10-332-447-10
Sequence 10, Application US/10332447
Publication No. US20040053258A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; RAUMANN, Brigitte E.;
APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
APPLICANT: TANG, Y. Tom; HARLAND, Lee; BURFORD, Neil;
APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;
APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;
APPLICANT: HAFALIA, April J.A.; TRIBOULEY, Catherine M.;
APPLICANT: WALSH, Roderick T.; RAMKUMAR, Javalaxmi;
APPLICANT: LU, Yan; LU, Dyung Aina M.; AZIMZAI, Yalda;
APPLICANT: LAL, Preeti; ELLIOTT, Vicki S.; NGUYEN, Dannel B.;
APPLICANT: XU, Yuming; SEILHAMER, Jeffrey J.; BOROWSKY, Mark L.;
APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANGAVELU, Kavitha;
APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: PI-0149 USN
CURRENT APPLICATION NUMBER: US/10/332,447
CURRENT FILING DATE: 2003-01-07
PRIORITY APPLICATION NUMBER: US 60/216,547
PRIORITY FILING DATE: 2000-07-07
PRIORITY APPLICATION NUMBER: US 60/218,232
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 60/220,112
PRIORITY FILING DATE: 2000-07-21
PRIORITY APPLICATION NUMBER: US 60/221,839
PRIORITY FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 724
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040053258A1 7472728CDI
US-10-332-447-10

78 VAIFVVVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHAL 137
133 DADNAGVSPIGNSSNNSSHDWLGSAFFAGTAVTTITIGYGNIAPTSEGGKIFCILYAIQFI 192
138 DADNAGVSPIGNSSNNSSHDWLGSAFFAGTAVTTITIGYGNIAPTSEGGKIFCILYAIQFI 197
193 PLFGELLAGIGDQLGTIFGKSIARVEKVFRRKQVSQTKIRVISTITLFIAGCIVFVTIPA 252
198 PLFGELLAGIGDQLGTIFGKSIARVEKVFRRKQVSQTKIRVISTITLFIAGCIVFVTIPA 257
253 VIFKYIEGWTALESYIFVVTITTTVGDFVAGNAGINREYWKPLVWFWLVLGLAYPA 312
258 VIFKYIEGWTALESYIFVVTITTTVGDFVAGNAGINREYWKPLVWFWLVLGLAYPA 317
313 AVLSMIGDMLVLSKTKKEEVEGTEKAAHAAEWKANTVAFRETRRRLSVIEIHDKLOAAATI 372
318 AVLSMIGDMLVLSKTKKEEVEGTEKAAHAAEWKANTVAFRETRRRLSVIEIHDKLOAAATI 377
373 RSMERRRLGLDQRAHSLDMLSPKESVFAALDTGRFKASSQESINNRPNLRLKGPQOLN 432
378 RSMERRRLGLDQRAHSLDMLSPKESVFAALDTGRFKASSQESINNRPNLRLKGPQOLN 437
433 KHGQASSEDNIINKFGSTSRITKRNKDKLKTLPEDVOKIYKTPRYNSLDEKKSEETSK 492
438 KHGQASSEDNIINKFGSTSRITKRNKDKLKTLPEDVOKIYKTPRYNSLDEKKSEETSK 497
493 MCNSDSSSTAMLTDCIQOHAELNGMIPTDKREPENNLSLEDEN 538
498 MCNSDSSSTAMLTDCIQOHAELNGMIPTDKREPENNLSLEDEN 543
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Query Match 96.3%; Score 2657.5; DB 15; Length 724;
Best Local Similarity 98.7%; Pred. No. 1.3e-207;
Matches 523; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

QY 13 VAVPAAAPVCPQKSAATNGQPPAPPTPTPLRSSRATVVARMEGTSQGLQTVMKWKT 72
DB 196 VAVPAAAPVCPQKSAATNGQPPAPPTPTPLRSSRATVVARMEGTSQGLQTVMKWKT 255

QY 73 VAIFVVVVVLTGGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHAL 132
DB 256 VAIFVVVVVLTGGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHAL 315

QY 133 DADNAGVSPIGNSSNNSSHWDLSGAPFPAGTIVTTIGYNIAPSTEGKIFCILYAI 192
DB 316 DADNAGVSPIGNSSNNSSHWDLSGAPFPAGTIVTTM-YGNIAPSTEGKIFCILYAI 374

QY 193 PLFGFLLAGIGDQGTIFGKSIARVEKVPKQVQSOTKIRVISTILFILAGCIVFTTIP 252
DB 375 PLFGFLLAGIGDQGTIFGKSIARVEKVPKQVQSOTKIRVISTILFILAGCIVFTTIP 434

QY 253 VIFKYIEGTALLESYFVVVLTITVGFDFVA---GGNAGINRYEWKPLVWFILVGL 308
DB 435 VIFKYIEGTALLESYFVVVLTITVGFDFVAVVVFGRNAGINRYEWKPLVWFILVGL 494

QY 309 AYFAAVLSMIGDMLRVLSKKTKEVGEIKAHAAEWKANVTAEFRTRRLSVEIHDKLQR 368
DB 495 AYFAAVLSMIGDMLRVLSKKTKEVGEIKAHAAEWKANVTAEFRTRRLSVEIHDKLQR 554

QY 369 AATRSERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNLRLKGP 428
DB 555 AATRSERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNLRLKGP 614

QY 429 EQLNKHGGASSEDNIINKFGSTSLTKRKNKDLAKTLPEDVQKIYKTFRNTSLDEEKEE 488
DB 615 EQLNKHGGASSEDNIINKFGSTSLTKRKNKDLAKTLPEDVQKIYKTFRNTSLDEEKEE 674

QY 489 ETEKMCSDNSSTAMLTDCIQOHAELNGMIPTDTKOREPENNLSLEDN 538
DB 675 ETEKMCSDNSSTAMLTDCIQOHAELNGMIPTDTKOREPENNLSLEDN 724

RESULT 8
US-09-729-920-5
; Sequence 5, Application US/09729920
; Patent No. US20020103115A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000858
; CURRENT APPLICATION NUMBER: US/09/729,920
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-729-920-5

Query Match 92.8%; Score 2560.5; DB 9; Length 538;
Best Local Similarity 95.4%; Pred. No. 6.8e-200;
Matches 503; Conservative 9; Mismatches 8; Indels 7; Gaps 2;

QY 13 VAVPAAAPVCPQKSAATNGQPPAPPTPTPLRSSRATVVARMEGTSQGLQTVMKWKT 71
DB 18 VAVPAAAPVCPQKSAATNGH-----HPVPLRSSRATVVARMEGASQGLQTVMKWKT 71

QY 72 VVAIFVVVVVLTGGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHA 131
DB 72 VVAIFVVVVVLTGGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHA 131

QY 132 LDADNAGVSPIGNSSNNSSHWDLSGAPFPAGTIVTTIGYNIAPSTEGKIFCILYAI 191
DB 132 LDADNAGVSPIGNSSNNSSHWDLSGAPFPAGTIVTTIGYNIAPSTEGKIFCILYAI 191

QY 192 IPLFGFLLAGIGDQGTIFGKSIARVEKVPKQVQSOTKIRVISTILFILAGCIVFTTIP 251
DB 192 IPLFGFLLAGIGDQGTIFGKSIARVEKVPKQVQSOTKIRVISTILFILAGCIVFTTIP 251

QY 252 AVIFKYIEGTALLESYFVVVLTITVGFDFVAGNAGINRYEWKPLVWFILVGLAYF 311
DB 252 AVIFKYIEGTALLESYFVVVLTITVGFDFVAGNAGINRYEWKPLVWFILVGLAYF 311

QY 312 AAVLSMIGDMLRVLSKKTKEVGEIKAHAAEWKANVTAEFRTRRLSVEIHDKLQRAAT 371
DB 312 AAVLSMIGDMLRVLSKKTKEVGEIKAHAAEWKANVTAEFRTRRLSVEIHDKLQRAAT 371

QY 372 IRSERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNLRLKGP 431
DB 372 IRSERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNLRLKGP 431

QY 432 NKHGGASSEDNIINKFGSTSLTKRKNKDLAKTLPEDVQKIYKTFRNTSLDEEKEE 491
DB 432 NKHGGASSEDNIINKFGSTSLTKRKNKDLAKTLPEDVQKIYKTFRNTSLDEEKEE 491

QY 492 KVCNDSNSTAMLTDCIQOHAELNGMIPTDTKOREPENNLSLEDN 538
DB 492 KVCNDSNSTAMLTDCIQOHAELNGMIPTDTKOREPENNLSLEDN 538

RESULT 9
US-09-828-746-6
; Sequence 6, Application US/09828746
; Patent No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6

Query Match 45.2%; Score 1248.5; DB 9; Length 411;
Best Local Similarity 64.3%; Pred. No. 4.5e-93;
Matches 247; Conservative 53; Mismatches 67; Indels 17; Gaps 5;

QY 17 AAAPVCPQKSAATNGQPPAPPTPTPLRSSRATVVA-RMEGTSQGLQTVMKWKTVAI 75
DB 2 AAPDLLDPKSA-----AQNSKPLSPSPKPTVLASRVESDS---AINVMKWKTVSTI 50

QY 76 FVVVVVLTGGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHALDAD 135
DB 51 FLVVVLTGGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHALDAD 110

QY 136 NAGVSPIGNSSNNSSHWDLSGAPFPAGTIVTTIGYNIAPSTEGKIFCILYAI 195
DB 111 NAGVSPIGNSSNNSSHWDLSGAPFPAGTIVTTIGYNIAPSTEGKIFCILYAI 170

QY 196 GFLLAGIGDQGTIFGKSIARVEKVPKQVQSOTKIRVISTILFILAGCIVFTTIP 255
DB 196 GFLLAGIGDQGTIFGKSIARVEKVPKQVQSOTKIRVISTILFILAGCIVFTTIP 255

Db 171 GFLLAGVGDQGTIFGKIAKVEDTPIKWNVSQTKIRIISTITIFILFGCVLFVALPAVIF 230
QY 256 KYIEGWTALSIYFVVVTLTTVGFDFVAGGNAGINRYEYKPLVWFWLVLGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYVVTITTTIGFGDYVAGG-SDIEYLDYFYPVWFWLVLGLAYFAAVL 289
QY 316 SMIGDMLRVLSKTKKEEVEGEIKAHAAEWKANTVTAEPRETRRLSVIEIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEEVEGEFRAHAAEWANTVTAEPKTRRLSVIEIYDKFORATSV--- 346
QY 376 ERRRLGLDORAHSLDMLSPKRSV 399
Db 347 -RRKLSAELAGNHNOELTPCMTL 369

RESULT 10

US-09-892-360-18
; Sequence 18, Application US/09892360
; Publication No. US20040101833A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: ROMEY, GEORGES
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-892-360-18

Query Match 45.0%; Score 1243; DB 11; Length 411;
Best Local Similarity 62.7%; Pred. No. 1.3e-92;
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;
QY 17 AAAPVCQPKSATNGOPPAPAPTPTPLRSLSSRATVVA-RMEGTSQGGLOTVMKKTVAI 75
Db 2 RAPDLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKKTVSTI 50
QY 76 FVVVVYLVGTGLVFRALBPPESSQKNTIALEKAEFLRDHVCVSPQELTILQHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKTFISQHSVCNSTELDELIIQIIVAI 110
QY 136 NAGVSPIGNSSNNSSHDLGSAFFPAGTVTTTIGYGNIAPISTEGGKIFCIIYAIPIPLF 195
Db 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYALLGIPLF 170
QY 196 GFLLAGIGDQGTIFGKIAKVEDTPIKWNVSQTKIRIISTITIFILAGCIVFVTPAVIF 255
Db 171 GFLLAGVGDQGTIFGKIAKVEDTPIKWNVSQTKIRIISTITIFILFGCVLFVALPAIIF 230
QY 256 KYIEGWTALSIYFVVVTLTTVGFDFVAGGNAGINRYEYKPLVWFWLVLGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYVVTITTTIGFGDYVAGG-SDIEYLDYFYPVWFWLVLGLAYFAAVL 289
QY 316 SMIGDMLRVLSKTKKEEVEGEIKAHAAEWKANTVTAEPRETRRLSVIEIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEEVEGEFRAHAAEWANTVTAEPKTRRLSVIEIYDKFORATSV--- 346
QY 376 ERRRLGLDORAHSLDMLSPKRSV 399
Db 347 -RRKLSAELAGNHNOELTPCMTL 369

RESULT 11

US-09-828-746-2
; Sequence 2, Application US/09828746
; Patent No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-2

Query Match 45.0%; Score 1242.5; DB 9; Length 411;
Best Local Similarity 63.5%; Pred. No. 1.4e-92;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;
QY 17 AAAPVCQPKSATNGOPPAPAPTPTPLRSLSSRATVVA-RMEGTSQGGLOTVMKKTVAI 75
Db 2 RAPDLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKKTVSTI 50
QY 76 FVVVVYLVGTGLVFRALBPPESSQKNTIALEKAEFLRDHVCVSPQELTILQHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKTFISQHSVCNSTELDELIIQIIVAI 110
QY 136 NAGVSPIGNSSNNSSHDLGSAFFPAGTVTTTIGYGNIAPISTEGGKIFCIIYAIPIPLF 195
Db 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYALLGIPLF 170
QY 196 GFLLAGIGDQGTIFGKIAKVEDTPIKWNVSQTKIRIISTITIFILAGCIVFVTPAVIF 255
Db 171 GFLLAGVGDQGTIFGKIAKVEDTPIKWNVSQTKIRIISTITIFILFGCVLFVALPAIIF 230
QY 256 KYIEGWTALSIYFVVVTLTTVGFDFVAGGNAGINRYEYKPLVWFWLVLGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYVVTITTTIGFGDYVAGG-SDIEYLDYFYPVWFWLVLGLAYFAAVL 289
QY 316 SMIGDMLRVLSKTKKEEVEGEIKAHAAEWKANTVTAEPRETRRLSVIEIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEEVEGEFRAHAAEWANTVTAEPKTRRLSVIEIYDKFORATSV--- 346
QY 376 ERRRLGLDORAHSLDMLSPKRSV 399
Db 347 -RRKLSAELAGNHNOELTPCMTL 369

RESULT 12
US-10-121-746-83
; Sequence 83, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 411
TYPE: PRT
ORGANISM: H. sapiens
US-10-121-746-83

Query Match 45.0%; Score 1242.5; DB 14; Length 411;
Best Local Similarity 63.5%; Pred. No. 1.4e-92;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCPKSNATNGQPAPAPPTPRLSSSRATVVA-RMEGTSQGLQTVMKWKTVAI 75
Db 2 AAPDLLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKKTSTI 50
QY 76 FVVVVVYLTGVLVFPALQEPSSQKNVIALEKAEFLRDHVCVSPQLETLIOHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAI 110
QY 136 NAGVSPIGNSSNNSSHWDLGSAFFPAGTIVTTIGYGNIASTEGGKIFCILYAIPIPLF 195
Db 111 NAGIPLGNISNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYALLGPIPLF 170
QY 196 GFLLAGIGDQGTIFGKSIARVEKVFKEQVSTQKIRIVSTIFILAGCIVFVTPAVIF 255
Db 171 GFLLAGVGDQGTIFGKGIKVEDTPIKNVSTQKIRIISTIFILFGCVLFVALPAIIP 230
QY 256 KIEGWTALLESYFVVVLTGFGDFVAGNAGINREWYKPLVWFWILVGLAYFAAVL 315
Db 231 KHIEGWSALDAIYFVVVLTGFGDYVAGG-SDIEYLDYKPVVWFWILVGLAYFAAVL 289
QY 316 SMIGDLRLVLSKTKKEEVEGEIKAHAAEWKANTVABPRETRRLSVEIHDKLOAAATIRSM 375
Db 290 SMIGDLRLVISKTKKEEVEGEFPAHAAEWNTVABFEKTRRLSVEIYDKFORATSI--- 346
QY 376 ERRRLGLDQRAHSLDMSPEKRSV 399
Db 347 -KRKLSAELAGNHQELTFCRRTL 369

RESULT 13
US-10-745-210-2
Sequence 2, Application US/10745210
Publication No. US20040143855A1
GENERAL INFORMATION:
APPLICANT: TONONI, Giulio
APPLICANT: CIRELLI, Chiara
TITLE OF INVENTION: ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS
FILE REFERENCE: 054030-0044
CURRENT APPLICATION NUMBER: US/10/745,210
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US 60/436,201
PRIOR FILING DATE: 2001-12-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-10-745-210-2

Query Match 45.0%; Score 1242.5; DB 16; Length 411;
Best Local Similarity 63.5%; Pred. No. 1.4e-92;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCPKSNATNGQPAPAPPTPRLSSSRATVVA-RMEGTSQGLQTVMKWKTVAI 75

Db 2 AAPDLLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKKTSTI 50
QY 76 FVVVVVYLTGVLVFPALQEPSSQKNVIALEKAEFLRDHVCVSPQLETLIOHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAI 110
QY 136 NAGVSPIGNSSNNSSHWDLGSAFFPAGTIVTTIGYGNIASTEGGKIFCILYAIPIPLF 195
Db 111 NAGIPLGNISNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYALLGPIPLF 170
QY 196 GFLLAGIGDQGTIFGKSIARVEKVFKEQVSTQKIRIVSTIFILAGCIVFVTPAVIF 255
Db 171 GFLLAGVGDQGTIFGKGIKVEDTPIKNVSTQKIRIISTIFILFGCVLFVALPAIIP 230
QY 256 KIEGWTALLESYFVVVLTGFGDFVAGNAGINREWYKPLVWFWILVGLAYFAAVL 315
Db 231 KHIEGWSALDAIYFVVVLTGFGDYVAGG-SDIEYLDYKPVVWFWILVGLAYFAAVL 289
QY 316 SMIGDLRLVLSKTKKEEVEGEIKAHAAEWKANTVABPRETRRLSVEIHDKLOAAATIRSM 375
Db 290 SMIGDLRLVISKTKKEEVEGEFPAHAAEWNTVABFEKTRRLSVEIYDKFORATSI--- 346
QY 376 ERRRLGLDQRAHSLDMSPEKRSV 399
Db 347 -KRKLSAELAGNHQELTFCRRTL 369

RESULT 14
US-09-939-484-8
Sequence 8, Application US/09939484
Patent No. US20020032322A1
GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 1201-CIP-DIV-00
CURRENT APPLICATION NUMBER: US/09/939,484
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/144,914
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 08/749,816
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: FR 96/01565
PRIOR FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 370
TYPE: PRT
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: TREK-1
US-09-939-484-8

Query Match 44.9%; Score 1238.5; DB 9; Length 370;
Best Local Similarity 64.2%; Pred. No. 2.5e-92;
Matches 246; Conservative 52; Mismatches 68; Indels 17; Gaps 5;

QY 17 AAAPVCPKSNATNGQPAPAPPTPRLSSSRATVVA-RMEGTSQGLQTVMKWKTVAI 75
Db 2 AAPDLLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---AINVMKKTSTI 50
QY 76 FVVVVVYLTGVLVFPALQEPSSQKNVIALEKAEFLRDHVCVSPQLETLIOHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFIAQACVNSTDELIIQIVAAI 110
QY 136 NAGVSPIGNSSNNSSHWDLGSAFFPAGTIVTTIGYGNIASTEGGKIFCILYAIPIPLF 195

Db 111 NAGIIPLGSSNQVSHWDLGSSFFTAGTITIGFNGISPRTEGKIFCIYALLGIPLE 170
Qy 196 GFLLAGIGDOLGTIFGKSTARVEKVKQVOTKIRVISTILFILAGCIVFTIPAVIF 255
Db 171 GFLLAGVGDLGTIFGKIAKVEDTFIKWNSQTKIRIISTITIFILFGCVLVALPAVIF 230
Qy 256 KYIEGWTALESIYFVVVTLTTVGDFVAGGNAGINREWKPLVWFWILVGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYFVITLTTIGFDYVAGG-SDIEYLDIFYKPVVFWILVGLAYFAAVL 289
Qy 316 SMIGDMLRVLSKTKKEEVEIKAHAAEWKANTAFRETRRLSVEIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEEVEIFRAHAAEWNTAFBKTETRRRLSVEIYDKFORATSV--- 346
Qy 376 ERRRLGLDQRAHSLDMLSPKES 398
Db 347 -KRKLSAELAGNHNOELTPCMT 368

RESULT 15

US-09-939-483-8
; Sequence 8, Application US/09939483
; Patent No. US2002009458A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-939-483-8

Query Match 44.9%; Score 1238.5; DB 9; Length 370;
Best Local Similarity 64.2%; Pred. No. 2.5e-92;
Matches 246; Conservative 52; Mismatches 68; Indels 17; Gaps 5;
Qy 17 AAAPVCPKSAATNGQPPAPPTPELSTSSRATVVA-RMEGTSQGLQTVNKKTVVAI 75
Db 2 AAPDLDPKSA-----AQNSKPLSFSSKPTVLASRVSDS---AINVMKTKVTSTI 50
Qy 76 FVVVVVYLVGTGLVFRALQPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDAD 135
Db 51 FLVVVLYLIIGAFAVKALQPOEISQRTTIVIQKTFIAQHACVNSTELDELIQIVRAI 110
Qy 136 NAGVSPIGNSSNNSHWDIGSAFFPAGTITIGYNIAPSTEGKIFCIYALFGIPLE 195
Db 111 NAGIIPLGSSNQVSHWDLGSSFFTAGTITIGFNGISPRTEGKIFCIYALLGIPLE 170
Qy 196 GFLLAGIGDOLGTIFGKSTARVEKVKQVOTKIRVISTILFILAGCIVFTIPAVIF 255
Db 171 GFLLAGVGDLGTIFGKIAKVEDTFIKWNSQTKIRIISTITIFILFGCVLVALPAVIF 230
Qy 256 KYIEGWTALESIYFVVVTLTTVGDFVAGGNAGINREWKPLVWFWILVGLAYFAAVL 315

Db 231 KHIEGWSALDAIFYFVITLTTIGFDYVAGG-SDIEYLDIFYKPVVFWILVGLAYFAAVL 289
Qy 316 SMIGDMLRVLSKTKKEEVEIKAHAAEWKANTAFRETRRLSVEIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEEVEIFRAHAAEWNTAFBKTETRRRLSVEIYDKFORATSV--- 346
Qy 376 ERRRLGLDQRAHSLDMLSPKES 398
Db 347 -KRKLSAELAGNHNOELTPCMT 368

Search completed: April 28, 2005, 13:41:12
Job time : 136 secs

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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:22:27 ; Search time 42 Seconds
(without alignments)
1232.491 Million cell updates/sec

Title: US-09-892-360-2
Perfect score: 2760
Sequence: 1 MFPLYTDFLSLVAVPAAAP.....IPTDTKOREPNNLSLEDRN 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	403	14.6	336	2	inward rectifier p
2	329	11.9	330	2	TASK-5 protein - h
3	326	11.8	1001	2	potassium channel
4	315.5	11.4	329	2	probable potassium
5	307	11.1	336	2	outward rectifier
6	300.5	10.9	364	2	probable potassium
7	298.5	10.8	393	2	hypothetical prote
8	298.5	10.8	1910	2	protein t12C9_3 [i
9	290.5	10.5	334	2	hypothetical prote
10	282.5	10.2	392	2	hypothetical prote
11	268.5	9.7	522	2	hypothetical prote
12	265.5	9.6	528	2	hypothetical prote
13	264.5	9.6	444	2	hypothetical prote
14	264	9.6	551	2	hypothetical prote
15	262.5	9.6	555	2	potassium channel
16	262.5	9.5	443	2	hypothetical prote
17	260.	9.4	461	2	potassium channel
18	258.5	9.4	513	2	hypothetical prote
19	255	9.2	452	2	hypothetical prote
20	252.5	9.1	586	2	hypothetical prote
21	248	9.0	325	2	hypothetical prote
22	247	8.9	427	2	hypothetical prote
23	245	8.9	1136	2	hypothetical prote
24	244	8.8	504	2	hypothetical prote
25	233.5	8.5	484	2	probable potassium
26	233.5	8.5	519	2	hypothetical prote
27	233.5	8.5	1539	2	hypothetical prote
28	229.5	8.3	383	2	hypothetical prote
29	227.5	8.2	307	2	protein twk-24 [im

30 224.5 8.1 524 2 T23907 hypothetical prote
31 224.5 8.1 769 2 T27550 hypothetical prote
32 221.5 8.0 643 2 T26616 hypothetical prote
33 218 7.9 335 2 S44635 f22b7.7 protein -
34 217.5 7.9 691 2 S46585 outward-rectifier
35 216.5 7.8 576 2 T43363 potassium channel
36 213.5 7.7 660 2 T21551 hypothetical prote
37 213 7.7 569 2 T43531 probable potassium
38 210.5 7.6 544 2 T43364 potassium channel
39 208.5 7.6 485 2 T24201 hypothetical prote
40 207.5 7.5 700 2 T27364 hypothetical prote
41 204.5 7.4 550 2 T22557 hypothetical prote
42 203.5 7.4 539 2 T23700 hypothetical prote
43 202 7.3 681 2 T19429 hypothetical prote
44 198 7.2 631 2 T26232 hypothetical prote
45 189.5 6.9 475 2 T27725 hypothetical prote

ALIGNMENTS

RESULT 1

S65566
inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65566
R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Roney, G.; Barhanin, EMO J. 15, 1004-1011, 1996
A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel A:Reference number: S65566; MUID:96183184; PMID:8605869
A:Accession: S65566
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: UNIPROT:O00180; EMBL:U33632; NID:gi086490; PIDN:AAB01688.1; PID:gl

Query Match 14.6%; Score 403; DB 2; Length 336;
Best Local Similarity 33.2%; Pred. No. 2e-20;
Matches 95; Conservative 53; Mismatches 104; Indels 34; Gaps 9;

Qy 76 FVVV-VVYLVGSLVFALEQPPSSQKNTALEKAEFLRDHVCVSPQELTFLIHALD 133
Db 25 FLVLGYLLYVFGAVFSSVELPYEDLLRQLRKLKRFLSEHECLSSQQLQPLGRVLE 84
Qy 134 ADNAGVSPIGNSSNNSSHWDLGSAFFAGTITITIGYGNIAFSTEGGKIFCLLYAIFGIP 193
Db 85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLTGTGYHTVPLSDGKRAFCIIYSVIGIP 143
Qy 194 LFGFLLAGIGDQLGTIFGKSTARVEKVRKKQV-----SQTIRIVSTIL--FILA 242
Db 144 FTLLFLTAV-----VQRTVTVTRPVLYFHIRWGFQKQVAVIAVLGLGVTV 192
Qy 243 GCIVFVTIPAVIFKYIE-GWTALESIIYFVVVLTITVGFDFVAGNAGINRYEWYKPLVW 301
Db 193 SCPPF--IPAAVFSVLEDDNNFLSFYCFISLTIGLDVVPBGYNQKRELKYIGIT 250
Qy 302 FWILVGLAYFAVLISMGLMRLVLSK-----KTEEVGEIKAAHAE 342
Db 251 CYLLGLLIAMLVLETFCB-LHELKFRKRMFYVKKDKEDQVHIIE 295

RESULT 2

JC7703
TASK-5 protein - human
C:Species: Homo sapiens (man)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: JC7703
R:Kim, D.; Gnatenco, C.
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A:Title: TASK-5, a new member of the tandem-pore K+ channel family.
A:Reference number: JC7703; MUID:21303050; PMID:11409881
A:Accession: JC7703

A:Molecule type: DNA
A:Residues: 1-330 <KIM>
A:Cross-references: GB:AL118522
C:Comment: This protein, a new member of the tandem-pore K⁺ channel family with four transmembrane domains, is secreted by the cell but does not produce a functional plasma membrane K⁺ current by itself.
C:Genetics:
A:Gene: task-5
A:Map position: 20q12
C:Keywords: transmembrane protein
F:107-128/Domain: transmembrane segment #status predicted <TMS1>
F:129-155/Region: hydrophobic cytoplasmic linker #status predicted
F:156-180/Domain: transmembrane segment #status predicted <TMS3>
F:220-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match 11.9%; Score 329; DB 2; Length 330;
Best Local Similarity 32.4%; Pred. No. 2.6e-15;
Matches 85; Conservative 46; Mismatches 97; Indels 34; Gaps 9;

QY 75 IFVVVVVYLVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQSELETLIQHALDA 134
DB 11 LVLTCTCLLVGAADFALSAEASGRQR-LLVQKRGALRRKFGFSAEDYRELRLALQA 69
QY 135 D--NAGVSPIGNSSNNSHDGLSAPFAGTIVTTIGYGNAPSTEGGKIFCILYAFGI 192
DB 70 EPHRAG-----RQMKFGSGFYFAITVTTIGYGHAAAGTDSGKVFVYALIGI 118
QY 193 PLFGLLAGIGDGLTIFGKSTARVEKVRKQVQSQTIRIVSTILFILAAG--CIVFVT 249
DB 119 PLTVTFQSLGERLNAV-----VRLI--LLAAKCCGLRWCVTSTENLVVAGLACAATLA 172
QY 250 IPAVIEKIEGTALLESIFVVTTLTGVGDFVA--GGNAGINRYREWYKPLVFWFVLVG 307
DB 173 LGAVAFSHFEGWTFHAYYCYFITLTTIGFGDFVALQGEA-LQRKLPYVAFSFLYILG 231
QY 308 LAYFAAVLSMI-----GDW 321
DB 232 LTVIGAFNLVVLFLVASADW 253

RESULT 3
T13807
potassium channel protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
A:Accession: T13807
R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from Drosophila
A:Reference number: Z17770; MUID:97075152; PMID:8917578
A:Accession: T13807
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1001 <GOL>
A:Cross-references: UNIPROT:Q94526; EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AAC692
C:Genetics:
A:Gene: ORK1
A:Cross-references: FlyBase:FBgn0017561
A:Map position: 1

Query Match 11.8%; Score 326; DB 2; Length 1001;
Best Local Similarity 22.9%; Pred. No. 1.8e-14;
Matches 123; Conservative 93; Mismatches 193; Indels 128; Gaps 20;

QY 68 KKTVAIFVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQSELETL 127
DB 5 RW---ILLIFVISYLMFGAAIYTHIEGEEK-----ISRAQRKAQIAINEYLLEL 54
QY 128 -----IQHALDADNAGVSPIGNSSNNSHDGLSAPFAGTIVTTIGYGNAPSTEGGKIFCI 176
DB 55 GKNTTQDEILQRIQSDYCDKPVTLPTDPTDPTWTFHAFHFAFTVCSTVGIGNIST 114
QY 177 TEGGKIFCILYAFGIPLFGLLAGIGDGLTIFGKSTARVEKVRKQVQSQTIRIVSTILFILAAG 230

DB 115 TFAGRMIMIAYSVIGIPVNGILFAGLGE-----YFGRTPEAIYRYRYKCYKMSDTHYVPPQ 170
QY 231 IRVITLILF-LACGIVFVTPAVIFKYIEGTALLESIFVVTTLTGVGDFVA--GGN 287
DB 171 LGLITVVIAIIPGALFLLPSWVFFYFENWPYSISLYSVYVTTTIGFGDYVTFPGAN 230
QY 288 AGINRYEW---YKPLVFWFVLVGLYFAAVLSMIGDWLRVLSKK-----TKEEVGSIKAHA 340
DB 231 QPKFEGGWVYQIFVIFWIFSLGLVIMWTFITRGLQ--SKLAYLEQQLSNLTATQ 288
QY 341 AEWKANTVAETRETRRLS-----VEIHDKLQRAATIRSMERRR-----LGL 382
DB 289 NRIWSGVTQKGVYLRRLNELYILKVPYVTDVIAITLPRSNSCPDLSMTYRVEPAPIS 348
QY 383 DORASL--DMLSPKRS--VFAALDTGRFKASSQSSINNRP-----NNLRK 425
DB 349 RKRAFSCADNVAQREAGWTHANSDBTSLKLDREKTFETAAYRQTTDLAKVVALAT 408
QY 426 KGP-----EQLNKRG--QGASEDNI-----INFGSTSRLTFRKKNKDLKTLPE-- 467
DB 409 VKPPAEQEDAAALYGVHGFSDSOLASEWSFSTWNEPTSPRRPRARACSDFNLEAPRWQ 468
QY 468 -----DVQKIYKTFRN-----YSLDEKKEEETEK 492
DB 469 SERPLRSHNEWTSGDNQIOEAFNORYKQORANGAANSTWVHLBPDALBEOLEK 525

RESULT 4
T43509
probable potassium channel chain n2P38 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
A:Accession: T43509
R:Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450
A:Accession: T43509
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-329 <WAN>
A:Cross-references: UNIPROT:O17185; EMBL:AF083652; PIDN:AAC32863.1

Query Match 11.4%; Score 315.5; DB 2; Length 329;
Best Local Similarity 31.6%; Pred. No. 2.2e-14;
Matches 86; Conservative 48; Mismatches 99; Indels 39; Gaps 9;

QY 73 VAIFVVVVVYLVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQSELETL----- 127
DB 9 LSLIVCTLTLLVGAADFALSAEASGRQR-LLVQKRGALRRKFGFSAEDYRELRLALQA 67
QY 128 --IQHALDADNAGVSPIGNSSNNSHDGLSAPFAGTIVTTIGYGNAPSTEGGKIFCI 185
DB 68 KSVPH-----KAGY-----QWKPGAFYFATVTTIGYGHSTPMTDAGKVF 111
QY 186 LYAIFGIPFGFLAGIGDGLTIFGKSTARVEKVRKQVQSQTIRIVSTILFILAAG----- 241
DB 112 LYALAGIPLGLIMFGSICGERWNTFAKLLRIRRAAGKQPI-----VTSSDLIFCTGW 165
QY 242 AGCIVFVTPAVIFKYIEGTALLESIFVVTTLTGVGDFVAGNAG-INRYEWYKPLV 300
DB 166 GGLLIFG--GAFMFSYENWTYFDAVYCYFVTLTTIGFGDYVALQKRGSLQTOPEYVPS 223
QY 301 WFWILVGLYFAAVLSMIGDWLRVLSKKTKEE 332
DB 224 LVFILFGLTVISAAMNLL--VLRFLTMNTEDE 253

RESULT 5
T32347
outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: F32347
R/Murray, J.; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A/Description: The sequence of C. elegans cosmid F34D6.
A/Reference number: Z21153
A/Accession: F32347
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-336 <WUR>
A/Cross-references: UNIPROT:O17185; EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:
A/Experimental source: strain Bristol N2; clone F34D6
C/Genetics:
A/Gene: twk-23; CESP:F34D6.3
A/Map position: 2
A/Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match	11.1%;	Score 307;	DB 2;	Length 336;
Best Local Similarity	30.3%;	Pred. No. 8.e-14;		
Matches	84;	Conservative 50;	Mismatches 101;	Indels 42; Gaps 9

QY	73	VAIFVVVVVYLVTVGGLVPRALRQPFSSQKQTIALEKAEPLRDHVCSQPSQLETLIQHAL	132
DB	9	LSLVCTLTLYLVGAARFADALETENBILQVRGLG-----EPRKLQVRREKL	55
QY	133	----DADNAG-----VSPIGNSSNNSSHWDLGSAFFFACTVTTTIGYGNIAPESTGG	180
DB	56	KTKYNNMADYEILRATIVKSPHKA--GYQWKPSGAFYATVTTTIGYGHSTPMTDAG	113
QY	181	KIFCILYAFGIPFGFLLAGIGDQLGTIFGKSIARVEKVRKKQVSQTKIRVISTILFI	240
DB	114	KVFCMLYALAGIPGLIMFQSIGERMNTFAAKLRFIRRAKGQPI-----VTSSDLII	167
QY	241	L-----AGCIVFVTPVAVIFKYIEGWTALESIFYVVVLTLTTVGFGFVAGGNAG--INTYRE	295
DB	168	FCYCWGGLLIYG--GAPMFSSYENWNTYDVAVYCFVTLTTIGFGDYVALQKRSIQTQPE	225
QY	296	YKPLVWFWILVGLYAFPAVLNMGIDWLRLVSKTKBE	332
DB	226	YVFFSLVFLIFGLTVISAAAMLL--VLRFLTWNTDE	260

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RESULT 6
T43361
probable potassium channel chain n2p20 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43361
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450
A:Accession: T43361
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-364 <WANG>
A:Cross-references: UNIPROT:076790; EMBL:AF083646; PIDN:AAC32857.1

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	Query Match	10.9%; Score 300.5; DB 2;	Length 364;
	Best Local Similarity	26.8%; Pred.No 2.8e-13;	
	Matches	106; Conservative 78;	Mismatches 124; Indels 87; Gaps 19;
QY	70 KTVVAIPVVV--VVLVTGGIVFALRQPFPSSOKNTIALEKAEFLRDHV---- <td>123</td> <td></td>	123	
	:	: : :	: : :
	:	: : :	: : :
	:	: : :	: : :
Dd	7 KSARALLIILSTFTYLFGAMVFQKLE-----SEKTWVRDEIRITDRLKHKNFSERD	61	
	:	: : :	: : :
	:	: : :	: : :
QY	124 LETLIQHLDADNAGVSPIGNSSNSSHWDLGSAFFAGTAVTTIGYNIAPIAPTEGGRKF	183	
	:	: : :	: : :
	:	: : :	: : :
Dd	62 L-----HLPEA--IAIKSIPOQA--GYCMQAFAGFYATVITTVYGHSAPSINAGKL F	112	
	:	: : :	: : :
	:	: : :	: : :
QY	184 CIIFYAIPIGFELPGLLAGIDQLGTIFPKSJARVEKVFRK-----KQVSOTKI RVIS-T	236	
	:	: : :	: : :
	:	: : :	: : :
Dd	113 CMTFAIFGVPMGLIMFOISIGERVNTFYAISLHKFERDSLHOOGFTCLCBQEVTFHLLMYSLT	172	
	:	: : :	: : :
	:	: : :	: : :

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Qy      237 ILF--ILAGCIVFTIPAVIFKYIEGWTALESIYPVVVLTITVGPGDFVAGNAGINyre 294
Db      173 IGFMIIVSGTYMFT-----IEKWSIFDAYIFYCMITFTSIGFDLVP--LQQVNALQ   222
Qy      295 WYKPLVMVF---WTLVLGLAVFAAFLSMIGDWMLRVLSKTKTESEVGEIKAHAAEWKANVTAE 350
Db      223 -DQLIYVFATIMFLIGLAVFSACVNLH-----VLGFMASNADE----VTAA 264
Qy      351 FRE-----TRRRLSVEIHDKLQRAATIRSMERRRLGLIDORAHSLDMLS----- 393
Db      265 QREPPSAIVLERFTNSLVDSQIFNIQKHSVTGVLP----GRPREMYSIVPNSTADVHLR 320
Qy      394 --PEKRSVPAALDTGRFKASSQE---SINNRPNNL 423
Db      321 RRSTRRSIQDTCVCGCFKP RP RHFRFSLTRPTNI 355

RESULT 7
T25392
hypothetical protein T28A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25392
R:11Novd C
```

submitted to the EMBL Data Library, March 1997

A;Reference number: Z20027

A;Accession: T25392

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-393 <WIL>

A;Cross-references: UNIPROT:Q9XU07; EMBL:Z28113; PIR

A;Experimental source: clone T28A8

C;Genetics:

A;Gene: CRSP:T28A8.1

A;Map position: 3

A;Introns: 73/1 112/3; 179/2; 209/3; 287/2; 310/3;

Query Match	10.8%	Score	298.5	DB 2	Length	393			
Best Local Similarity	27.1%	Pred. No.	4.2e-13						
Matches	85	Conservative	50	Mismatches	94	Indels	85	Gaps	11
QY	69	WKTIV-----VAIFVVVVVYLTGGIVFRALEQPPSSQKNTALEKASFLRDHVCVSP	121						
DB	4	WKTARIILAHVLSLVSVYVYGAFPLFQLEQP	53						
QY	122	QLETLIQIALDADNAGVSP-----IG-----NSSNNS	149						
DB	54	-HKRQMLEHLWENRESGIGHVVEDLAVKYVDNVRILFEAPDTHCIGAKHLRPGGDE	112						
QY	150	SHWDLGSAFFAGTVTTTIGYGNIAPESTGGKIFCILYAIFGPLFGFLAGIGDQLGTI	209						
DB	113	YNNVTYMTALPFTTLLTTTIGYGNLTPTVGRGKLLCILYALFGVPL-----ILITVAD-IGKF	168						
QY	210	FGKSIARVEKVPK-KQVSTQKIRIVST-----ILFILAAGCI	245						
DB	169	LSENIVOLVITWYHKLREKSKQKYSVISSKDDRNKSGDLMLDHLNYSIPILFVAILL	228						
QY	246	VFTTIPAVIFKYITEGHTALESIFYVVVVTLTTVFGGDFVAGGNAGINREYWKPLVFWFWIL	305						
DB	229	SYITFGAVLSMWEGWDFFSGFFPSFITMTVVGFIIVP-----LKREYY-ILDLCCYII	281						
QY	306	VGLAYFAAVLSMIG	319						
DB	282	IGLSITTMCIDLVG	295						

RESULT 8
H88124
protein T12C9.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;date: 10-May-2001 #sequence_revision 10-May-2001
C;Accession: H88124

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: AY5000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <STO>
A:Cross-references: GB:chr_II; PIDN:AC71141.1; PID:gl086770; GSPDB:GN00020; CESP:T12C9.3
A:Note: proline-rich
C:Genetics:
A:Gene: T12C9.3
A:Map position: 2

Query Match 10.8%; Score 298.5; DB 2; Length 1910;
Best Local Similarity 21.2%; Pred. No. 3.3e-12;
Matches 121; Conservative 90; Mismatches 197; Indels 163; Gaps 22;
QY 10 LSLVAPPAAPVCPQKSAATNGOPAP-APT-TPRLSSSRATVVARMECTSQGLQT 65
DB 134 LSFSTPATRKACLEKQV---HPPIHETPPQFGRFRSIFGLLESARPDDETTTLQN 190
QY 66 VMKWTV---VAIFVVVVVLTGGLVPRALQEPFESSQK-----NTIALEKA----- 110
DB 191 IRKYAKLALPHIVLVVCIVATIGAWIFVTLESFNEDELKTKTGRKTIAMESNLIYKIN 250
QY 111 -----EPLRDHVCVSQEL-----EYLIQHA-----LDADNAGVSPIGN 144
DB 251 NNEKEVWKEDIEKELMYSEKLYKAFKQYVRYSDVTITGFGSRSEYEADETG---GD 306
QY 145 SNNSSH-----NDLGSARFFAGVITVIGYGNIASTEGGKIFCILYALF 190
DB 307 SERKRHRHGNKRGDRGSEKMTTSSALFPAAITWATIGIGNIVPTPLGLACVLFLP 366
QY 191 GIPLFGFLAGIDQGLG--TIF-----GKSIARVEKVRK----- 223
DB 367 GAPIAITIGDLGKFLSECTWLYKHMKGSRALDSAMKFRGLEDSISDDLESASKQD 426
QY 224 -----KQVSTKIRVISTILFILAGCIVFTTIPAVIFKTYEGWTALESYFVVVILT 275
DB 427 SSILDMDMDEIDKSEVPVLMVFTIIL---LYTAFGGILFLEDSYMDAFYFISIT 482
QY 276 TVGFGDFVAGGNAGINREWRKPLVFWLVLGLVPAAVLSMIG----- 319
DB 483 TIGFGDIVPENHD-----YTAIMLIYLGVLGVSTTMCIDLAGIQYIKIHFGRKFG 535
QY 320 -DMLRVLSKTK-----EVGEIKAHAAEMKANYTABFRTTRRLSLVSIHDKLQR 368
DB 536 TDLQVLYKKRMLERLANGQGEILRYKHVAVE-----KFEREQEQLOQKMBEEDPP 588
QY 369 AATIRSMERRRGLDQRAHSL-----DMLSPKRSV---FAALTGRPKASQES 415
DB 589 STESKGFDMRIRIDSLSAFQLRFYDTYDEEDLFSFTIHSVRSFQPSVMSHSSARSQS 648
QY 416 I---NNRPNNLKGPELNKKGQASQSEDN 443
DB 649 CRPQRNGASWDESGP-SUSEHCSLSTEPSV 678

RESULT 9

T19860
hypothetical protein C40C9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19860
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19860
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.1
A:Map position: X
A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 10.5%; Score 290.5; DB 2; Length 334;
Best Local Similarity 28.6%; Pred. No. 1.2e-12;
Matches 89; Conservative 67; Mismatches 94; Indels 61; Gaps 15;
QY 70 KTVVAIFVVV---VVLVTGGLVPRALQEPFESSQKNTIALEKAEPLRDHV---CVSPQES 123
DB 7 KSARALLILSTFTYLLFGAMVFDKLE-----SEKDTWVRDEIRITDLRKHKYFNSRD 61
QY 124 LETLIQHALLADNAGVSPIGNSSNNSSHWDLGSAFFRAGTITVITGYNIAPISTEGGKIF 183
DB 62 L-----HLFEA--TAIKSIPQOA--GYQWQFAGAPYFATVITVITVGYGHSAPSTNAGKLF 112
QY 184 CILVAIFGIFLFGFLLAGIGDQGLTIFGKSIARVEKVRK-----KQVSTKIRVIS--T 236
DB 113 CMIFALFGVFMGLMFQSIGERVNTFIAYSLHKFRDSLHQOQFTCLQEVTPHLLMVSIT 172
QY 237 ILF--ILAGCIVFTTIPAVIFKTYEGWTALESYFVVVLTITVVGDFVAGGNAGINRE 294
DB 173 IGFVIVSGTYMFT-----IEKWSIFDAYYFCMITFTSTIGFGDLVP--LQOVNALQ 222
QY 295 WYKPLVWF-----WILVGLAYFAANVLDMTGMWLVLSKTKSEVGEIKAHAAEMKANYTAB 350
DB 223 -DQPLVFEATTMFLIGLAVSACVNL-----VLGFMASNADE-----VTAA 264
QY 351 PRETRRRRLSVE 361
DB 265 QREPPSAIVLE 275

RESULT 10

T45032
hypothetical protein Y39B6.f [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45032
R:Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berke, M.; Bonfield, J.; Burton, R.; Wilson, R.; Fulten, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johraser, A.; Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994
A:Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonhammer, S.; tock, L.; Wilkinson-Sproat, J.; Wohlman, P.
A:Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A:Reference number: S43531; MUID:94150718; PMID:7906398
A:Accession: T45032
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-392 <WIL>
A:Cross-references: EMBL:AL132896; NID:g6434440; PIDN:CAB60911.1; PID:g6434446
A:Experimental source: clone Y39B6B
C:Genetics:
A:Map position: 3
A:Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
A:Note: Y39B6.f

Query Match 10.2%; Score 282.5; DB 2; Length 392;

Best Local Similarity 31.7%; Pred. No. 5.3e-12;
Matches 77; Conservative 46; Mismatches 97; Indels 23; Gaps 8;
QY 90 FRALQEPFESSQKNTIALEKAEFLRDHVC---VSPQELTIQHALLADNAGVSPIGNSS 146
DB 118 FSRIEVPLEKIEREAY-LDYQNMWRDLIQLDDESEDKLF--LNIREAALINGWMWR 173
QY 147 NNSS---HWDLGSAPFFAGTITVITGYNIAPISTEGGKIFCILYALFIPFLLAGIGD 204
DB 174 NLTSDPNWTFGQAFPGTFLISTVGYGRVSPRTEYKGLFTILYCVIGIPLTLLALLSAIVA 233

QY 205 QL-----GTIFGKSIAIEKVKRQVQSTKIRVI--STILFILAGCIVFTIPAVIFKVI 258
DB 234 RMREPSHKLRLGLNORLGHFLTWNHQLIHVGVPASLLLFVFA-----IPAWVFSS 286
QY 259 B-GWTALESIIYFVVVTLTTVGGDFVAGGAGNINREWKPLVFWILVGLYFAAVLSM 317
DB 287 ETDWSLDAPFYCFVSLTTIGLDFPDPGDPNQSGFRGLYKIGATVYLMGGLCQMLPLAT 346
QY 318 IGD 320
DB 347 LYD 349

RESULT 11
T24265
hypothetical protein T01B4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24265
R:Wilkinson, J.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19866
A:Accession: T24265
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-522 <WIL>
A:Cross-references: UNIPROT:Q22042; EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4
A:Experimental source: clone T01B4
C:Genetics:
A:Gene: CESP:T01B4.1
A:Map position: X
A:Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match 9.7%; Score 268.5; DB 2; Length 522;
Best Local Similarity 22.3%; Pred. No. 7.2e-11;
Matches 120; Conservative 89; Mismatches 181; Indels 147; Gaps 21;

QY 73 VAIFVVVVVYLVGTGLVFRALF---QPPE-----SSQKNTALEKAEFLRDHVCVSP 121
DB 39 IWLIIILGACLGGMFQALBYDQOOLEAEKRVLSSESLLAVNLEHLKQVNCQS 98
QY 122 QB-----LETLIHALDADNAGVSPICGNSSNNSHWDLSGAPFAGTIVTTIGYGNIA 174
DB 99 NEKRCLELITKTFIQRSEEREG-----WRWDPWNSVFSSATIPTTIGYGNLA 147
QY 175 PSTEGGKIPCIILYAFGLPLGFLAGIDQGLTIFGKSI-----ARVEKVKRQVQST 229
DB 148 KTNLGRITATIIYGMIGIPLMLFVLNFG-ELCVKWKAKIQPNVQOCLKCKFCGRKQKAS 206
QY 230 KIRVIST-----ILPLAGCIVFTIPAVIPKVIKGTWALESIY 268
DB 207 SLASITKEMLEVPFEVDEDDKEDTTFQLRWGLLVILFVLCSPVSVFWENWDLTAPY 266
QY 269 FVVTLTTVGGDFVAGGAGNINREWKPLVFWIL--VGLAYFAAVLSMIGD----- 320
DB 267 FPFVSLSTIGFDIVP-----DHPTACALFVLYFGLALFAMVYAILQEVENQY 317
QY 321 -W-LRVLSKKYKEEVEIKAHAAEWA---NVTAEFRTRRLSV--EIHDKLQRAATIRSM 375
DB 318 MWALELDQYOEKLKODMYDEDEKADKNDMHFSKPEVRGPRILLQD--LLRGPDLKIS 376
QY 376 ERLRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGP-EQLNKH 434
DB 377 GGRSSSD--ASSVITEASDE-----DTRHFKV-----GRAILAEAPADERASNH 420
QY 435 QGASEDNIINKFGSTSLTRKKNKDLKTLPEDEVQKIYKTRF-----NYSLDEEK 485
DB 421 GTQLNSCTVSNHSDSC-----QIEAIVFSHFPTSFNFQNFYSSDSSL 463
QY 486 KEETERKCNLS-----DNSSTAM-----LTDCTQHAELNG 517
DB 464 EEHQLEYDNTSGTPPPYGDPTTTFNQTREDTIVSLAEKTPLSLMLKMLEEENDENG 520

RESULT 12

T21834
hypothetical protein F36A2.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21834
R:Lennard, N.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19476
A:Accession: T21834
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-528 <WIL>
A:Cross-references: UNIPROT:P90863; EMBL:Z81077; PIDN:CAB03071.1; GSPDB:GN00019; CESP:1
A:Experimental source: clone F36A2
C:Genetics:
A:Gene: CESP:F36A2.4
A:Map position: 1
A:Introns: 45/3; 81/3; 114/3; 151/3; 195/1; 306/1; 326/1; 368/2; 413/1; 464/2; 494/1

Query Match 9.6%; Score 265.5; DB 2; Length 528;
Best Local Similarity 22.2%; Pred. No. 1.2e-10;
Matches 122; Conservative 86; Mismatches 163; Indels 179; Gaps 26;

QY 79 VVYLVTCGLVFRALF-----QPPE-----SSQKNTALEKA 110
DB 25 VLYIILGAIIVFQMLEGHLNDFDNPKKHFGPKQVNDKFFETIFRRWSKGAN---FKKS 81
QY 111 EFLRDHVCVSPQ-----ELETILI-----QHALDADNAGVSP 142
DB 82 ALKDDHMAKIQNAKYDYDKLWSVAKRDRDKYKVNVEDLIKSVKEDTVDVDFVTVFA 141
QY 143 -----GNSSNNSHWDLSGAPFAGTIVTTIGYGNIAPISTEGGKIFCIILYAFGLPFG 197
DB 142 HRAVRHGYDESDPTWDPANSVFTTTMLTSLTIGYGVAPSTFGRLFGVYICLIGIPLTLV 201
QY 198 LLAGIGDGLG-TIP-----GKSIARVEKVKRQVQST 232
DB 202 TVANVAKPLSETIIFLHYELNWKLEWKRK--RKEGEVADPLQPMFGDDENESEILDRVR 259
QY 233 VIS-----TILFILAGCIVFTIPAVIPKVIKGTWALESIYFVVVTLTTVGGDF--VAGN 287
DB 260 LVREPLTVFPFV--FVYGCIAWVRYWNTWTVESLYIFIFISILTVGGDIRPSPGN 316
QY 288 AGINREWKPLVWF--WILVGLAYFAAVLSMIGD-----LRVLSKTKKEE-----VGE 335
DB 317 -----IWTLLAFVVVGVILTTMCMDVVGRMYLKEIHYLGRKLKSSNPFPYLLRE 364
QY 336 IKAHAAEWKANVTAEFRTRRLSV-----EIHDKLQRAATIRSMRRL 380
DB 365 AKAR-----RRAAMASLLAQLAKGMIFAHDYNELARKKSKRKEKR- 408
QY 381 GLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGP-EQLNKHQCGASE 440
DB 409 -----GSHVL-----PNEKMFARLPD--PPSDCQVSTSAVSVRLWAPPF-----SP 451
QY 441 D-----NIINKFGSTSLTRKKNKDLKTLPEDEVQKIYKTRFNYSLDEEKKEEETKMC- 494
DB 452 DPDLTYNIRYRLNATAVFKDQQRSPLSALFIKTDKI--EFHKCVGHGSKETIDVDSICE 509
QY 495 NSDSSSTAML 504
DB 510 KEDNETTALL 519

RESULT 13

T26229
hypothetical protein W06D12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26229

A;Map position: X
A;Introns: 14/3; 65/3; 95/2; 118/1; 165/3; 267/1; 297/2; 334/3; 385/2; 477/1; 513/2

	Query Match	9.6%;	Score 264;	DB 2;	Length 551;	
	Best Local Similarity	20.3%;	Pred. No. 1.6e-10;			
	Matches 108;	Conservative	94;	Mismatches 205;	Indels 124;	Gaps 16;

Qy 74 AIFVVVVVYLTGGLFRALSQPFESSOKNTALEKAEFLRDHVCVSPOELEYL----- 127
 : : : : :
Db 24 SLLMLVLLSPLGGFIPDRIETNAHAEMK-----RNERINRTACVS-QILHSIRWSHN 76
 : : : : :
Qy 128 ----IQHALDADNAGVSPIGNSNNSHWDLGSAPFFACTGVITTTGYGNIAPSTEGGKIP 183
 : : : : :
 : : : : :

Qy	184	CILYALFIPFLPGLLAGIQDQGLTTPGKSIARVEKVRKQVSGTKI-----RVIS	235
Db	133	CIVYGICGIPVMTIIIANVGOYLNNFAGDSRRKIEAYRQORRMKSASLAGKIYKESSIQV	192
Qy	236	TILFILAGCIVFTIPIAVIPKYIEG-WTALESYFVVTLLTTVCGDFVAGNAGINVRE	294
Db	193	TSALLCVFIIYAVGALLPLLLNGELDFNGLYFNFLCLTAIDFGQLVP-----IRV	245
Qy	295	WYKPLWFWFIIVLGLA-----YFAAVLSIMGDMLR	323
Db	246	ELLPIITFLYCYIGLAITTAINTGSEYMKLHYWGKKHNAAOQTRIFPGGKTLKVRDLLH	305
Qy	324	VLSKKTKEVEGETKAHAAEKANKVTAFTRETRRLSVEIHDKLQRAATIRSM-----	375
Db	306	AVGKKCVGFGMIDALDENVVERTIANQSGREP-PEDLNDEPPREPSRPIIHSPCSTR	364
Qy	376	-----ERRRLGIDQRAHSLDMLSPKRSVFAALDTGRFKASS	412
Db	365	PSNPPMSPSPREDHPPIFKMDAPAPRSPPLPAYELDI---KKPIFOALSNEPMQSA	420
Qy	413	QESINNRPNNLRLK-GPEQLNKH-----GOGASEDNII---NKFGSTSRLLTKR	456
Db	421	QEXLFDNDLTFQIEINTELVEDHKCSBVIIEPPATFEDMTIQHSLCVEDYERBEKVPCK	480
Qy	457	KNKDLKTLTPEDVQKIYKTPFNYSLDSEKKEETEKKMCNSDNSSTAMLTDC	507
Db	481	-FREKKEMYGRDPRKLYET---YQEBWDRLERLSDRKHGPPRKSVNLINSNC	527

A;Accession: I13357
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-555 <WAN>
A;Cross-references: UNIPROT:Q20673; EMBL:AF083645; PIDN:AAC32856.1

Query Match 9.6%; Score 264; DB 2; Length 555;
Best Local Similarity 20.3%; Pred. No. 1.6e-10;
Matches 108; Conservative 94; Mismatches 205; Indels 124; Gaps 16

Qy 74 AIFVVVVVYLVTGLVFRALEQPPESSQNTIALEKAEFLRDHVCVSQPLETL----- 127
 | :
Db 28 SLMLVLVLYSLGFGFIDRIETNAHEMK-----RNERINRTACVS-QILHSIHRWSHN 80

Qy 128 ----IQALADNAGVSPIGNSSNNSHWDLGSAFFPAGTIVITTYGYNIAPSTGGKIF 183
 | :
Db 81 QTHKVQVAEDIADC----FEPEKDERSEWNFTVLTLYGFIVITLGYNRIADIYTGRRP 136

Qy 184 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSARVEKVPKKQVQSOTKI-----RVIS 235

```
Db 137 CUVYICIGIPVTMIIANVQYLNFPAGDSRRKIEAYQOORMSKASLAGKIYKESSIQV 196
Qy 236 TILFILAGCIVFVTIPAVIFKYIEG-WTALESIIYFVVTLTTVGFQDFVAGGNAGINTYRE 294
Db 197 TSLALLCVFLIYVAVGALLPLLLNGELDFNGLYFNFLCLTAIDFGQLVP-----IRV 249
Qy 295 WYKPLVWFILVGLA-----YFAAVLSMIGDWLR 323
Db 250 ELLPITFLYVCIGLAITTIAINIGSEYMKKLYHWGKKMKNAQAOTRIWFGGKTLKVRDLLH 309
Qy 324 VLSKKTKEEVGRIKAHAAEWKANVTAEPRETRRLSVEIHDKLRQAATIRSM----- 375
Db 310 AVGKCGVEPGMIDLDLENVVERTIAMQEGREP-PEDLNDEPPPREPSRSTIHSPCSTR 368
Qy 376 -----ERRRLGDORAHSLDMLSPEKRSVFAALDTGRFKASS 412
Db 369 PSNPMPSPSPREDHPFIFKMDAPAPRSPPLPAYELDI-----KKPIFQALSNEPMQSA 424
Qy 413 QESINNRPNLRLK-GPEQLNKH-----GQASBDNII-----NKFGSTSRLLTKR 456
Db 425 QEKLFDLDTTQIEINTELBVEDHKCESVIIIEPPATFEDMTIQHSLCVEDYEREKVPKR 484
Qy 457 KNKOLKKTLPBDVQKIYKTFRNYSLDEKKGEETEKMCSNDSNSTAMLTDC 507
Db 485 -FREKKEMYGRDPKLYET---YQBEWDRLERLSDRKHGPRRKSVNLNSNC 531
```

Search completed: April 28, 2005, 13:26:02
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:22:27 ; Search time 180 seconds
(without alignments)
1530.548 Million cell updates/sec

Title: US-09-892-360-2

Perfect score: 2760

Sequence: 1 MFELYTDFFLSLVAVPAAAP.....IPTDTKREPNNLSLEDRN 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2760	100.0	538	1	C1WA_HUMAN
2	2697	97.7	543	2	Q6B014
3	2584.5	93.6	538	2	Q60834
4	2578.5	93.4	535	2	Q8BUW1
5	2560.5	92.8	538	1	C1WA_RAT
6	2180.5	79.0	453	2	Q8B2B0
7	2117	76.7	546	2	Q8BEY1
8	1251.5	45.3	411	1	C1W2_MOUSE
9	1251.5	45.3	414	2	Q6P6P9
10	1247.5	45.2	426	2	Q920B6
11	1244.5	45.1	411	2	Q8HY88
12	1242.5	45.0	411	2	Q9NRT2
13	1218.5	44.1	426	1	C1W2_HUMAN
14	983.5	35.6	241	2	Q9CX88
15	930	33.7	193	2	Q8BWJ6
16	812.5	29.4	393	1	C1W4_HUMAN
17	790	28.6	398	1	C1W4_MOUSE
18	778	28.2	397	2	Q92414
19	512	18.6	309	1	C1WG_HUMAN
20	504	18.3	294	2	Q6X6Z5
21	483	17.5	499	1	C1W5_HUMAN
22	478.5	17.3	502	2	Q9TK62
23	477	17.3	448	2	Q6PFU3
24	460	16.7	262	2	Q6X6Z3
25	454	16.4	257	2	Q80XE0
26	452	16.4	322	2	Q6X6Z4
27	447	16.2	184	2	Q8N4V5
28	424.5	15.4	341	2	Q8H2T2
29	403	14.6	307	2	Q80IT4
30	400	14.6	336	1	C1W1_HUMAN
31	400	14.5	336	2	Q922T2

32	398	14.4	336	2	Q8R454
33	395.5	14.3	336	2	Q99L99
34	392	14.2	332	1	C1WH_HUMAN
35	390.5	14.1	336	1	C1W1_MOUSE
36	382	13.8	259	2	Q02821
37	371.5	13.5	323	2	Q6PEI1
38	360	13.0	331	2	Q8AVI5
39	352.5	12.8	409	1	C1W3_MOUSE
40	352.5	12.8	411	1	C1W3_RAT
41	351.5	12.7	299	2	Q9QX34
42	350.5	12.7	365	1	C1W9_CAVPO
43	349.5	12.7	394	1	C1W3_HUMAN
44	349	12.6	396	2	Q923V6
45	348.5	12.6	318	1	C1WF_RAT

ALIGNMENTS

RESULT 1

ID_C1WA_HUMAN STANDARD; PRT; 538 AA.
AC P57789; Q8TDK7; Q8TDK8; Q9HB59;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).
GN Name=KCNK10; Synonyms=TREK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20435789; PubMed=1080510; DOI=10.1074/jbc.M002822200;
RA Lesage F., Terrenoire C., Romey G., Lazdunski M.;
RT "Human TREK2, a 2p domain mechano-sensitive K+ channel with multiple regulations by polyunsaturated fatty acids, lysophospholipids and Gs, Gi, and Gq protein-coupled receptors.";
RT J. Biol. Chem. 275:28398-28405(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C).
RX MEDLINE=21896087; PubMed=11897838;
RA Gu W., Schlichtthorl G., Hirsch J.R., Engels H., Karschin C., Karschin A., Derst C., Steinlein O.K., Daut J.;
RT "Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain potassium channel TREK-2.";
RL J. Physiol. (Lond.) 539:657-668(2002).
CC -!- FUNCTION: Outward rectifying potassium channel. Produces rapidly activating and non-inactivating outward rectifier K(+) currents. Activated by arachidonic acid and other naturally occurring unsaturated free fatty acids.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=A; Synonyms=TREK-2a;
CC IsoId=P57789-1; Sequence=Displayed;
CC Name=B; Synonyms=TREK-2b;
CC IsoId=P57789-2; Sequence=VSP_006697;
CC Name=C; Synonyms=TREK-2c;
CC IsoId=P57789-3; Sequence=VSP_006698;
CC -!- TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney isoform b is strongly expressed in kidney (primarily in the proximal tubule) and pancreas, whereas isoform c is abundantly expressed in brain.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

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Q8x454	cavia porce
Q99199	mus musculus
Q96t54	homo sapien
Q08581	mus musculus
Q02821	oryctolagus
Q6pe11	brachydanio
Q8avi5	xenopus lae
Q35111	mus musculus
Q54912	rattus norv
Q9q334	mus musculus
Q99158	cavia porce
Q14649	homo sapien
Q923V6	rattus norv
Q8x510	rattus norv

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CC EMBL; AF279890; AAG15191.1; -
CC EMBL; AF385399; AAL95705.1; -
CC EMBL; AF385400; AAL95706.1; -
CC EMBL; HGNC:6273; KCNK10.
DR MIM; 605873; -
DR GO; GO:0005267; P:potassium channel activity; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR InterPro; IPR003280; K-channel_2pore.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR003976; Trek channel.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW Potassium; Potassium channel; Transmembrane; Transport;
KW Voltage-gated channel.
FT DOMAIN 1 71
FT TRANSMEM 72 92
FT DOMAIN 154 180
FT TRANSMEM 182 202
FT DOMAIN 203 233
FT TRANSMEM 234 254
FT DOMAIN 263 294
FT TRANSMEM 299 319
FT DOMAIN 320 338
FT CARBOHYD 144 144
FT CARBOHYD 147 147
FT CARBOHYD 148 148
FT VARSPPLIC 1 12
FT FTID=VSP 006697.
FT MFPLYTDFPLSL -> MKFPIETPRKQVNDPK (in
FT isoform C).
FT FTID=VSP 006698.
FT E -> G (in Ref. 2).
FT CONFLICT 529 529
FT SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;
Query Match 100.0%; Score 2760; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1e-158;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFPLYTDFPLSLVAVPAAPVCPKSNATNGQPAPAPPTTPRLSSSRATVVARMEGTSQ 60
DB 1 MFPLYTDFPLSLVAVPAAPVCPKSNATNGQPAPAPPTTPRLSSSRATVVARMEGTSQ 60
QY 61 GGLQTVMKWKTVAIFVWVYVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVS 120
DB 61 GGLQTVMKWKTVAIFVWVYVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVS 120
QY 121 POELTLQHALDADNAGVSPICGNSNNSSHDLSAPFFAGVTITTYGNIAPSTGG 180
DB 121 POELTLQHALDADNAGVSPICGNSNNSSHDLSAPFFAGVTITTYGNIAPSTGG 180
QY 181 KIFCILYALFGPLFGELLAGDGLGTFGKSIARVEKVPKQVQSQTIRVISTILFI 240
DB 181 KIFCILYALFGPLFGELLAGDGLGTFGKSIARVEKVPKQVQSQTIRVISTILFI 240
QY 241 LAGCIVFVTIPAVIPKYGWGTALRSIYFVWVLTGFGDFVAGNAGINREWKPLV 300
DB 241 LAGCIVFVTIPAVIPKYGWGTALRSIYFVWVLTGFGDFVAGNAGINREWKPLV 300
QY 301 NFWILVGLAYPAALVSMIGDMLRVLSKTKKERVGBIKAHAAEWKANVTAFRETRRLSV 360
DB 301 NFWILVGLAYPAALVSMIGDMLRVLSKTKKERVGBIKAHAAEWKANVTAFRETRRLSV 360
QY 361 EHKDKLORATIRSMERRRLGDORAHSLDMLSPKRSVFALDTCGRFKASSQESINRRP 420
DB 361 EHKDKLORATIRSMERRRLGDORAHSLDMLSPKRSVFALDTCGRFKASSQESINRRP 420

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QY 421 NNLLKKGPEQLNKGQASGSDNIINKFGSTSRLLTKRKNKDKLKTLPEDVQKIYKTFRYS 480
DB 421 NNLLKKGPEQLNKGQASGSDNIINKFGSTSRLLTKRKNKDKLKTLPEDVQKIYKTFRYS 480
QY 481 LDEBKKEEETKMCNSDMSSTAMLTDCIQHAELENGMIPTDTKORPENNSLLEDRN 538
DB 481 LDEBKKEEETKMCNSDMSSTAMLTDCIQHAELENGMIPTDTKORPENNSLLEDRN 538

RESULT 2
Q6B014 PRELIMINARY; PRT; 543 AA.
ID Q6B014
AC Q6B014;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Potassium channel, subfamily K, member 10, isoform 3.
GN Name=KCNK10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Pooled tissue;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buote T., Max S.I., Wang J., Hsieh N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellon N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzhanovskii M.I., Skalska J., Smallus D.B., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
SEQUENCE FROM N.A.
TISSUE=Pooled tissue;
Director MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC075022; AAH75022.1; -
EMBL; BC075021; AAH75021.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; P:ion channel activity; IEA.
DR GO; GO:0005267; P:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K-channel_2pore.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR01255; NIR_SIRalpha_1/3.
DR InterPro; IPR003976; Trek channel.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 543 AA; 60110 MW; 17DBIAFAFAB07C46 CRC64;
Query Match 97.7%; Score 2697; DB 2; Length 543;
Best Local Similarity 100.0%; Pred. No. 6.7e-155;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 VAVPAAPVCPKSNATNGQPAPAPPTTPRLSSSRATVVARMEGTSQGLQTVMKWKTVA 72
DB 13 VAVPAAPVCPKSNATNGQPAPAPPTTPRLSSSRATVVARMEGTSQGLQTVMKWKTVA 72

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Best Local Similarity 94.3%; Pred. No. 9e-124;
Matches 433; Conservative 6; Mismatches 11; Indels 9; Gaps 3;

QY 1 MEPLTYDPL--SLVAVPAA--PVCOPKSAATGQPPAPAPTPTPLRSLSSSRATVVARMEG 57
DB 1 MYFSYIGYFFPLPLVAVPAAAPVCPKSAATG-----HPVPLRSLSSSRATVVARMEG 54

QY 58 TQGGLOTVMKWTVAIFVWVVLVTGGLVFRALFQPFSSQKNTIALEKAEFLRDHV 117
DB 55 ASQGGLOTVMKWTVAIFVWVVLVTGGLVFRALFQPFSSQKNTIALEKAEFLRDHI 114

QY 118 CVSPQLETLIHALDADNAGVSPIGNSSNNSHMDLGSAPFAGTIVITIGYNIAPST 177
DB 115 CVSPQLETLIHALDADNAGVSPVGNSSNNSHMDLGSAPFAGTIVITIGYNIAPST 174

QY 178 EGKIFCILYALFGLPLFGLAGIDGLGTIFGKSIAEVEKVKQVQSKIRVIST 237
DB 175 EGKIFCILYALFGLPLFGLAGIDGLGTIFGKSIAEVEKVKQVQSKIRVIST 234

QY 238 LFILAGCIVFVPIPAVIFKYIEGWTALFESYFVWVLTGFGDFVAGNAGINREWK 297
DB 235 LFILAGCIVFVPIPAVIFKYIEGWTALFESYFVWVLTGFGDFVAGNAGINREWK 294

QY 298 PLVFWILVGLYFAVAVLSNIGDWLRVLSKTKKEVGEIKAHAAEWKANVTAEPRETRR 357
DB 295 PLVFWILVGLYFAVAVLSNIGDWLRVLSKTKKEVGEIKAHAAEWKANVTAEPRETRR 354

QY 358 LSVEIHDKLORATIRSMERRRLGLDORAHSLDMLSPKRSVFAALDTRGFKASSOESIN 417
DB 355 LSVEIHDKLORATIRSMERRRLGLDORAHSLDMLSPKRSVFAALDTRGFKASSOESIN 414

QY 418 NRPNNLRKGPQLNKHGQAGSEDNINKFGSTSLTKR 456
DB 415 NRPNNLRKGPQLNKHGQAGSEDNINKFGSTSLTKR 453

RESULT 7
Q68EY1 PRELIMINARY; PRT; 546 AA.

AC Q68EY1
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE LOC446288 protein (Fragment).
GN Name=LOC446288;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.11002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters S.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RL Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC080069; AAH80069.1; --
DR InterPro: IPR003280; K-channel_2pore.
DR InterPro: IPR001622; K-channel_pore.
DR InterPro: IPR003976; Trek_channel.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01499; TREKCHANNEL.
FT NON TER 546
SQ SEQUENCE 546 AA; 60977 MW; AF6C7FB34AD34A06 CRC64;

Query Match 76.7%; Score 2117; DB 2; Length 546;
Best Local Similarity 78.8%; Pred. No. 7.8e-120;
Matches 419; Conservative 47; Mismatches 54; Indels 12; Gaps 5;

QY 13 VAVPAAAPVCP-----KSATNGQPPAPAPTPTPLRSLSSSRATVVARMEGTSQGLQTV 66
DB 18 VAVPAAVTPAPPPEPPSEPKNGHQHTTATPRMSVCGSRSLVSTMDNTS--SGLHSV 76

QY 67 MKWKTVAIFVWVVLVTGGLVFRALFQPFSSQKNTIALEKAEFLRDHVCSPOLEST 126
DB 77 MKWKTVAIFVWVVLVTGGLVFRALFQPFSSQKNTIALEKAEFLRDHVCSPOLEDA 136

QY 127 LIQHALDADNAGVSPIGNSSNNSHMDLGSAPFAGTIVITIGYNIAPSTEGKIFCIL 186
DB 137 LIKRAIDADNAGVSPIGNSSNNSHMDLGSAPFAGTIVITIGYNIAPSTEGKIFCIL 196

QY 187 YAIIGIPLFGLAGIDGLGTIFGKSIAEVEKVKQVQSKIRVISTILFILAGCIV 246
DB 197 YAIIGIPLFGLAGIDGLGTIFGKSIAEVEKVKQVQSKIRVISTILFILAGCIV 256

QY 247 FVTIPAVIFKTEGWTALFESYFVWVLTGFGDFVAGNAGINREWKVLPVFWILV 306
DB 257 FVTIPAVIFKTEGWTALFESYFVWVLTGFGDFVAGNAGINREWKVLPVFWILV 316

QY 307 GLAYFAAVLSMIGDWLRVLSKTKKEVGEIKAHAAEWKANVTAEPRETRRSLVEIHDKL 366
DB 317 GLAYFAAVLSMIGDWLRVLSKTKKEVGEIKAHAAEWKANVTAEPRETRRSLVEIHDKL 376

QY 367 QRAATIRSMERRRLGLDORAHSLDMLSPKRSVFAALDTRGFKASSOESINRPNRLRK 426
DB 377 QRAATIRSMERRRLGLDORAHSLDMLSPKRSVFAALDTRGFKASSOESINRPNRLRK 436

QY 427 GPEQLNKHGQAGSEDNINKFGS--TSRLTKRKNKGLKTLPEDEVOKIYKTFNYSLDEEK 485
DB 437 EAEQTLHGQGVSEDNINKFGSNNKSLTKRKNKGLKTLPEDEVOKIYKTFNYSVDEEK 496

QY 486 KEEETKCMKNSDNTSNTAMLTDCIOQHAELNGMIPTDKOREPENNSLLEDR 537
DB 497 KEDEDDTISTD---TATLSDFL-RHSIIENGSIPTNETKEEESHESKALLEEK 544

RESULT 8
C1W2 MOUSE
ID C1W2 MOUSE STANDARD; PRT; 411 AA.
AC P97438;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium

DE channel protein TREK-1) (Two-pore potassium channel TPCK1) (TREK-1 K+ channel subunit).

GN Name=Kcnk2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.

RC TISSUE=Brain;

RX MEDLINE=97157476; PubMed=9003761;

RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C., Lazdunski M.;

RT "Cloning, functional expression and brain localization of a novel unconventional outward rectifier K+ channel.";

RL EMBO J. 15:6854-6862(1996).

RN [2]

RP REVISIONS.

RC TISSUE=Brain;

RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C., Lazdunski M.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP ACTIVATION.

RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;

RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;

RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";

RL Nat. Neurosci. 2:422-426(1999).

CC -!- FUNCTION: Outward rectifying potassium channel.

CC -!- SUBUNIT: Homodimer (Potential).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: High expression in brain and lung. Also detected in kidney, heart and skeletal muscle. Not detected in liver. In the brain, highest expression in olfactory bulb, hippocampus and cerebellum.

CC -!- MISCELLANEOUS: Inhibited by barium. Activated by volatile general anesthetics such as chloroform, diethyl ether, halothane and isoflurane.

CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

CC -----

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CC -----

DR EMBL; U73488; AAC53005.2; -

DR MGD; MGI:109366; Kcnk2.

DR GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.

DR GO; GO:0005249; P:voltage-gated potassium channel activity; IDA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signaling; IDA.

DR GO; GO:0006813; P:potassium ion transport; IDA.

DR InterPro; IPR003280; K+channel 2pore.

DR InterPro; IPR001622; K+channel pore.

DR InterPro; IPR003976; Trek channel.

DR PRINTS; PR01333; 2PORECHANNEL.

DR PRINTS; PR01499; TREKCHANNEL.

KW Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transmembrane; Voltage-gated channel.

FT DOMAIN 1 46 Cytoplasmic (Potential).

FT TRANSMEM 67

FT DOMAIN 129 155 Pore-forming 1 (Potential).

FT TRANSMEM 157 177 Potential.

FT DOMAIN 178 207 Cytoplasmic (Potential).

FT TRANSMEM 208 228 Potential.

FT DOMAIN 238 268 Pore-forming 2 (Potential).

FT TRANSMEM 273 293 Potential.

FT DOMAIN 294 411 Cytoplasmic (Potential).

FT DOMAIN 378 411 Essential for chloroform and halothane

FT DOMAIN 354 411 sensitivity.

FT CARBOHYD 95 Required for basal channel activity.

FT CARBOHYD 119 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 119 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 411 AA; 45297 MW; 89976DDD103EPA05 CRC64;

Query Match 45.3%; Score 1251.5; DB 1; Length 411;

Best Local Similarity 64.3%; Pred. No. 1.2e-67;

Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCPKSNATNGPPAPAPPTPRLSISSRATVVA-RMEGTSGGLOTKWKTIVAI 75

Db AAPDLDPKSA-----AQNKPRLSFSSKPTVLASRVESDS---AINVMKWTVTI 50

QY 76 FVVVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQSELTILQHALDAD 135

Db FLVVVYLYLIGAAVFKALEQEPQEIISQRTTIVIQKTFIAQHACVNSTELDLQIVAAI 110

QY 136 NAGVSPIONSSNSHWDLGSAFFPAGTIVITIGYNTIAPSTEGGKIFCILYAIFGIPLF 195

Db NAGIIPLGSSNQVSHWDLGSSFPFAGTIVITIGYNTIAPSTEGGKIFCILYAIFGIPLF 170

QY 196 GFLLAGIGDGLGTIFGKSIARVKKVQKVSQTKIRVISTILFETLACIGVPTTNAVIF 255

Db GFLLAGIGDGLGTIFGKSIARVKKVQKVSQTKIRVISTILFETLACIGVPTTNAVIF 230

QY 256 KYIEGWTALSIYFVWVTLTTVGFDFVAGNAGINREWKPLVWFVILVGLAYFAAVL 315

Db KHIEGWSALDAIFYVWVTLTTVGFDFVAGNAGINREWKPLVWFVILVGLAYFAAVL 289

QY 316 SMIGDLRLVSKTKKEVEGEIKAHAAEKNVTAFFETRRRLSVEIHDKQRAATIRSM 375

Db SMIGDLRLVSKTKKEVEGEIKAHAAEKNVTAFFETRRRLSVEIHDKQRAATIRSM 346

QY 376 EERRLGDLORAHSLDMLSPKRSV 399

Db -KRKLSEALAGNHNOELTPCRRTL 369

RESULT 9

Q6P6P9 PRELIMINARY; PRT; 414 AA.

ID Q6P6P9

AC Q6P6P9; (Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Kcnk2 protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CSBL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzyzanski M.I., Skalska U., Smalls D.B., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Potassium channel subfamily K member 2.
 GN Name=Kcnk2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=22370953; PubMed=12368289; DOI=10.1074/jbc.M207233200;
 RA Enyeart J.J., Xu L., Danthi S., Enyeart J.A.;
 RT "An ACPH- and ATP-regulated background K⁺ channel in adrenocortical
 cells is TREK-1";
 RL J. Biol. Chem. 277:49186-49199(2002).
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
 (TC 1.A.1.8) family.
 DR EMBL; AY148474; AAN37591.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006811; F:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR003280; K:channel 2pore.
 DR InterPro; IPR001622; K:channel pore.
 DR InterPro; IPR003976; Trek channel.
 DR PRINTS; PR01333; 2PORECHANNEL.
 DR PRINTS; PR01499; TREKCHANNEL.
 DR KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;
 Query Match 45.1%; Score 1244.5; DB 2; Length 411;
 Best Local Similarity 63.5%; Pred. No. 3.1e-67;
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;
 QY 17 AAAPVCPKSNATNGQPAPAPPTPTPLRLSISRATVVA-RMEGTSGGGLQTVMKKTVAI 75
 DB 2 AAPLLDPKSA-----AQNKPRLSFTKPTVLASRVSDT---TINWKKTVSTI 50
 QY 76 FVVVVVYLVLTGGLVFRALAEQPFSSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDAD 135
 DB 51 FLVVVLYLIGATVFKALEQPHIEISQRTTIVIQKTFISQACVNSTELDELIOQIVAAI 110
 QY 136 NAGVSPICGNSSNNSHWDLGSAFFAGTAVTTTIGVGNAPSTEGGKIFCILYAFGIPLF 195
 DB 111 NAGIPLGNTSNQISHWDLGSSFPFAGTAVTTTIGVGNISPRTEGGKIFCIYALGILF 170
 QY 196 GFLLAGIGDQLTGTFKSIARVEKVRKQVSQTKIRVISTILFTLAGCIVPVVTPAVIF 255
 DB 171 GFLLAGVGDLGTITFGKIAKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPILF 230
 QY 256 KYIEGWTALIESIFYVVTITLVGDFVAGGNAGINREWKPLVFWILVGLAYFAAVL 315
 DB 231 KHIEGWSALDAIFYVVTITLVGDFVAGG-SDIEYLDYFKPVVFWILVGLAYFAAVL 289
 QY 316 SMIGDWLRVLSKTYEEVEGEIKAAAEKAWNTAFETRRRLSVEIHDKQRAATIRSM 375
 DB 290 SMIGDWLRVLSKTYEEVEGEFRAHAETANTVAFETRRRLSVEIYDKFQRTSI--- 346
 QY 376 EERRILGLDQRAHSLDMLSPKRSV 399
 DB 347 -KRKLASLAGNHNOELTPCRRTL 369
 RESULT 12
 Q9NRT2 PRELIMINARY; PRT; 411 AA.
 AC Q9NRT2
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Two-pore domain potassium channel TREK-1 (Potassium channel, subfamily
 K, member 2).
 GN Name=TREK-1; Synonyms=KCNK2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20244931; PubMed=10784345;
 RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,
 RA Medhurst A.D., Murdoch P., Chapman C.G.;
 RT "Cloning, localisation and functional expression of the human
 orthologue of the TREK-1 potassium channel";
 RL Pflugers Arch. 439:714-722(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Bobak S.A., McWhan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
 (TC 1.A.1.8) family.
 DR EMBL; AF171068; AAF89743.1; -
 DR EMBL; BC069462; AAH69462.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006811; F:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR003280; K:channel 2pore.
 DR InterPro; IPR001622; K:channel pore.
 DR InterPro; IPR003976; Trek channel.
 DR PRINTS; PR01333; 2PORECHANNEL.
 DR PRINTS; PR01499; TREKCHANNEL.
 DR KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 411 AA; 45494 MW; PDE40CAB21B42A1C CRC64;
 Query Match 45.0%; Score 1242.5; DB 2; Length 411;
 Best Local Similarity 63.5%; Pred. No. 4.1e-67;
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;
 QY 17 AAAPVCPKSNATNGQPAPAPPTPTPLRLSISRATVVA-RMEGTSGGGLQTVMKKTVAI 75
 DB 2 AAPLLDPKSA-----AQNKPRLSFTKPTVLASRVSDT---TINWKKTVSTI 50
 QY 76 FVVVVVYLVLTGGLVFRALAEQPFSSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDAD 135
 DB 51 FLVVVLYLIGATVFKALEQPHIEISQRTTIVIQKTFISQACVNSTELDELIOQIVAAI 110
 QY 136 NAGVSPICGNSSNNSHWDLGSAFFAGTAVTTTIGVGNAPSTEGGKIFCILYAFGIPLF 195
 DB 111 NAGIPLGNTSNQISHWDLGSSFPFAGTAVTTTIGVGNISPRTEGGKIFCIYALGILF 170
 QY 196 GFLLAGIGDQLTGTFKSIARVEKVRKQVSQTKIRVISTILFTLAGCIVPVVTPAVIF 255
 DB 171 GFLLAGVGDLGTITFGKIAKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPILF 230
 QY 256 KYIEGWTALIESIFYVVTITLVGDFVAGGNAGINREWKPLVFWILVGLAYFAAVL 315
 DB 231 KHIEGWSALDAIFYVVTITLVGDFVAGG-SDIEYLDYFKPVVFWILVGLAYFAAVL 289
 QY 316 SMIGDWLRVLSKTYEEVEGEIKAAAEKAWNTAFETRRRLSVEIHDKQRAATIRSM 375
 DB 290 SMIGDWLRVLSKTYEEVEGEFRAHAETANTVAFETRRRLSVEIYDKFQRTSI--- 346
 QY 376 EERRILGLDQRAHSLDMLSPKRSV 399
 DB 347 -KRKLASLAGNHNOELTPCRRTL 369

Db 51 FLVVLVLIIGATVFKALQEPHEISQRTTIVIQKTFISQHSVCNVELDELIQIIVAAI 110
 Qy 136 NAGVSPIGNSSNHHWDLGSAFFAGTIVITIGVNIAPSTEGGKIFCIIYAIIGIPLF 195
 Db 111 NAGIPLGNTSNQISHWDLGSAFFAGTIVITIGVNIAPSTEGGKIFCIIYAIIGIPLF 170
 Qy 196 GFLLAGIGDQGTIFGKISARVEKVRKQVSTQIRVISTITLFIAGCIVFTIPAVIF 255
 Db 171 GFLLAGVGDQGTIFGKIAKVEDTFIKWVSTQIRVISTITLFIAGCIVFTIPAVIF 230
 Qy 256 KYIEGWTALESYFVVTITLTVGDFVAGNAGINREYKPLVWFWLVLGLAYFAAVL 315
 Db 231 KHIEGWSALDAIFVVTITLTVGDFVAGNAGINREYKPLVWFWLVLGLAYFAAVL 289
 Qy 316 SMIGDLRLVSKTKKEVEGEIKAHAAEWKANTVABETRRRLSVEIHDKLOAATIRSM 375
 Db 290 SMIGDLRLVSKTKKEVEGEIFRAHAAEWNTVABETRRRLSVEIHDKLOAATIRSM 346
 Qy 376 ERRRLGLDQRAHSLDMLSPKRSV 399
 Db 347 -KRKLSAELAGNHQELTFCRRTL 369

RESULT 13

CIW2 HUMAN STANDARD; PRT; 426 AA.
 AC Q95069; Q9UN63;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore potassium channel TPCK1).
 GN Name=CKNK2; Synonyms=TREK, TREK1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+ channels";
 RL Nat. Neurosci. 2:422-426(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Outward rectifying potassium channel.
 CC -!- SUBUNIT: Homodimer (Potential).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- MISCELLANEOUS: Activated by volatile general anaesthetics such as chloroform, halothane and isoflurane.
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
 CC
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 CC
 CC EMBL; AF129399; AAD47569.1; -
 CC EMBL; AF004711; AAD01203.1; -
 CC Genew; HGNC:6277; KCNK2.
 CC MIM; 603219; -
 CC GO; GO:0016020; C:membrane; NAS.
 CC GO; GO:0015271; F:outward rectifier potassium channel activity; NAS.
 CC GO; GO:0006813; P:potassium ion transport; NAS.

DR InterPro; IPR003280; K-channel 2pore.
 DR InterPro; IPR001622; K-channel pore.
 DR InterPro; IPR003976; Trek channel.
 DR PRINTS; PR01333; 2PORECHANNEL.
 DR PRINTS; PR01499; TREKCHANNEL.
 KW Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transport; Voltage-gated channel.
 FT DOMAIN 1 61
 FT TRANSMEM 62 82
 FT DOMAIN 144 170
 FT TRANSMEM 172 192
 FT DOMAIN 193 223
 FT TRANSMEM 224 244
 FT DOMAIN 253 283
 FT TRANSMEM 288 308
 FT DOMAIN 309 426
 FT TRANSMEM 378 426
 FT DOMAIN 354 426
 FT CARBOHYD 110 110
 FT CARBOHYD 134 134
 FT CONFLICT 2 16
 FT CONFLICT 309 311
 FT CONFLICT 391 391
 FT CONFLICT 411 411
 SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;
 Query Match 44.1%; Score 1218.5; DB 1; Length 426;
 Best Local Similarity 62.8%; Pred. No. 1.2e-65;
 Matches 241; Conservative 58; Mismatches 68; Indels 17; Gaps 5;
 Qy 17 AAAPVCPQKSNATGPPAPAPPTPLRLSISRATVVA-RMEGTSQGLQTVNKKTVVAI 75
 Db 17 AAPDLLDPKSA-----AONKRLSFTKPTVLASRVESDT---TINVMKTVSTI 65
 Qy 76 FVVVVVLTGVLVFRALQEPFESSQKNITALEKAEFLRDHVCSPQBLETLIQHALDAD 135
 Db 66 FLVVLVLIIGATVFKALQEPHEISQRTTIVIQKTFISQHSVCNVELDELIQIIVAAI 125
 Qy 136 NAGVSPIGNSSNHHWDLGSAFFAGTIVITIGVNIAPSTEGGKIFCIIYAIIGIPLF 195
 Db 136 NAGIPLGNTSNQISHWDLGSAFFAGTIVITIGVNIAPSTEGGKIFCIIYAIIGIPLF 185
 Qy 196 GFLLAGIGDQGTIFGKISARVEKVRKQVSTQIRVISTITLFIAGCIVFTIPAVIF 255
 Db 186 GFLLAGVGDQGTIFGKIAKVEDTFIKWVSTQIRVISTITLFIAGCIVFTIPAVIF 245
 Qy 256 KYIEGWTALESYFVVTITLTVGDFVAGNAGINREYKPLVWFWLVLGLAYFAAVL 315
 Db 246 KHIEGWSALDAIFVVTITLTVGDFVAGNAGINREYKPLVWFWLVLGLAYFAAVL 304
 Qy 316 SMIGDLRLVSKTKKEVEGEIKAHAAEWKANTVABETRRRLSVEIHDKLOAATIRSM 375
 Db 305 SMIGDLRLVSKTKKEVEGEIFRAHAAEWNTVABETRRRLSVEIHDKLOAATIRSM 361
 Qy 376 ERRRLGLDQRAHSLDMLSPKRSV 399
 Db 362 -KRKLSAELAGNHQELTFCRRTL 384
 RESULT 14
 Q9CX88 PRELIMINARY; PRT; 241 AA.
 ID Q9CX88
 AC Q9CX88
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:301005K24 product:POTASSIUM CHANNEL SUBFAMILY K MEMBER
 DE 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog.
 GN Name=1700024D23R1k;


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RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK052327; BAC34939.1; -
DR GO; GO:0005216; F10n channel activity; IEA.
KW Ionic channel.
FT NON_TER
SQ SEQUENCE 193 AA; 22174 MW; 8CCBADA59BF60641 CRC64;
Query Match 33.7%; Score 930; DB 2; Length 193;
Best Local Similarity 93.8%; Pred. NO. 1.3e-48;
Matches 181; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 346 NVTAFRETRRLSVEIHDKLRATIRSMERRRLGLDQRAHSLDMLSPKESVFAALDT 405
Db 1 NVTAFRETRRLSVEIHDKLRATIRSMERRRLGLDQRAHSLDMLSPKESVFAALDT 60
QY 406 GRFKASSQESINRRPNLRLKGPQLNKGQASDNIIKFGSTSLTKRKNKDKKTL 465
Db 61 GRFKASSQESINRRPNLRLKGPQLNKGQASDNIIKFGSTSLTKRKNKDKKTL 120
QY 466 PEDVOKIYKTFRNYSLDEEKEETKMCNDSNLTDCIQQAELNGWIPDTDKD 525
Db 121 PEDVOKIYKTFRNYSLDEEKEETKMCNDSNLTDCIQQAELNGWIPDTDKD 180
QY 526 REPENNSLLEDRN 538
Db 181 QGLENNLSLEDRN 193
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